

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 14:08:00 ; Search time 4200.2 Seconds
(without alignments)
2746.659 Million cell updates/sec

Title: US-09-856-320A-2
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Fgapop 6.0 , Fgapext 7.0
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Searched: 2888711 segs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1523	100.0	1106	6	BD137019 Human CAS
3	1523	100.0	1158	6	AX016289 Sequence
4	1523	100.0	1158	6	BD137020 Human CAS
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6	1523	100.0	1204	6	AX358932 Sequence
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8	1523	100.0	1204	6	AX454622 Sequence
9	1523	100.0	1204	6	AX464372 Sequence
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RESULT 1

ALIGNMENTS

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ACCESSION     AX016287
VERSION       AX016287.1 GI:10041854
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS       Bruck C.E., Coche T., Cassart J.P. and Vinals-Bassols C.
TITLE         Human casp12 polypeptide, a serine protease
JOURNAL       Patent: WO 949055-A 1 30-SEP-1999;
               BRUCK CLAUDE ELYVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);
               COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTTA
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Score:        1523.00        Matches:      282
Percent Similarity: 100.00%   Conservative: 0
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QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLeuThraGLeuLeuGly 80
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DEFINITION Human CASB 12 polypeptide, a serine protease.
ACCESSION   BD137019
VERSION     BD137019.1 GI:32321964
KEYWORDS    JP 2002507425-A/1.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS     Bruck C.E.M., Cassart J.P., Coche T. and Bassols C.V.
TITLE       Human CASB 12 polypeptide, a serine protease
JOURNAL     Patent: JP 2002507425-A 1 12-MAR-2002;
               SMITHKLINE BEECHAM BIOLOGICALS SA
COMMENT
OS          Homo sapiens (human)
PN          JP 2002507425-A/1
PD          12-MAR-2002
PF          17-MAR-1999 JP 2000538015
PR          20-MAR-1998 GB 9806095.7
PI          CLAUDEINE ELYVIRE MARIE BRUCK, JEAN POL CASSART, THIERRY COCHE, PI
               CARLOTTA VINALS BASSOLS
PC          C12N15/09, A61K31/70, A61K38/00, A61P35/00, A61P37/02, C07K16/40,
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PC          C12N1/19, C12N1/21, C12N5/10, C12N9/64, C12P21/02, C12Q1/02, C12Q1/
               PC 68, G01N33/15,
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Score:        1523.00        Matches:      282
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:  100.00%        Indels:      0
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 VERSION AX016289.1 GI:10041855
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.

TITLE Human casb12 polypeptide, a serine protease
 JOURNAL Patent: WO 9949055-A 3 30-SEP-1999;
 BRUCK CLAUDE ELMIRE MARIE (BE); SMITHKLINE BEECHAM (BE);
 COCHE THIERRY (BE); CASSART JEAN FOL (BE); VINALS-BASSOLS CARLOTTA (BE)
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 VERSION BD137020.1 GI:23231965
 KEYWORDS JP 2002507425-A/2.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1158)
 AUTHORS Bruck,C.E.M., Cassart,J.P., Coche,T. and Bassols,C.V.
 TITLE Human CASB 12 polypeptide, a serine protease
 JOURNAL Patent: JP 2002507425-A 2 12-MAR-2002;
 SMITHKLINE BEECHAM BIOLOGICALS SA
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 PN JP 2002507425-A/2
 PD 12-MAR-2002
 PF 17-MAR-1999 JP 2000538015
 PR 20-MAR-1998 GB 9806095.7
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 CARLOTA VINLIS BASSOLS
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 Yoshida,S., Taniuchi,M., Suemoto,T., Oka,T., He,X. and Shiosaka,S.
 TITLE cDNA cloning and expression of a novel serine protease, TLSP
 JOURNAL Biochim. Biophys. Acta 1399 (2-3), 225-228 (1998)
 MEDLINE 98438738
 PUBMED 9765601
 REFERENCE 2 (bases 1 to 1186)
 Yoshida,S.
 TITLE Direct Submission
 AUTHORS Submitted (10-APR-1998) Shigetaka Yoshida, Department of Anatomy 1,
 Asahikawa Medical College, Midorigaoka Higashi 2-1-1, Asahikawa,
 Hokkaido 078-8510, Japan (E-mail: syoshida@asahikawa-med.ac.jp,
 Tel:81-166-68-2300, Fax:81-166-68-2309)
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OY	101	IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr	120
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QY	221	AlaSerValGlnGlnGlyGlyLysAspSerCysGlnIyAspSerGlyGlyProLeuVal	240
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QY	241	CysAsnGlnSerLeuGlnGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg	260
Db	746	TGTACACAGCTCTCTTCAAGGCAATATCTCTGGGGGCGAGATCGTGTGCATCACCCGA	805
QY	261	LysProGlyValTYrThrLysValCysLysTyxValAspTrpIleGlnGlnIuThrMetLys	280
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ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Godowski,P.D., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I.		
TITLE	Severed and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0193983-A 185 13-DEC-2001;		
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Db	70	AAGGAACCTGGGGCCGCTCTCTCCCTTCAGGCATAGAGATTCTGCAGTTATCTG	129
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REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watnabe,C.K. and Wood,W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0208288-A 185 31-JUN-2002;		
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REFERENCE 1
AUTHORS Baker, K. P., Ferrara, N., Gerber, H., Gerritsen, M. E., Goddard, A., Godowski, P. J., Gurney, A. L., Hillan, K. J., Masters, S. A., Pan, J., Peoni, N. F., Stephan, J. P., Watanabe, C. K., Williams, P. M., Wood, W. I., and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 207 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Masters, Scott A. (US) ; Pan, James (US) ; Peoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)
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ACCESSION AX464372
VERSION AX464372.1 GI:21899202
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K. P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E., Gao, W. Q., Gerritsen, M. E., Goddard, A., Godowski, P. J., Gurney, A. L., Sherwood, S., Smith, V., Stewart, T. A., Tumas, D., Watanabe, C. K., Wood, W. I., and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0140466-A 505 07-JUN-2001;
Genentech Inc. (US)
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DB 730 TGTAACTGATCTCTTCAAGGCAATATCTCTGCGGCCAGAGTCCGTGTGCGATCAACCGA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLys 280
DB 790 AAGCTGTGTGTACACAAAGTGTGCAAAATATGTGACTGTGATCCAGAGACGATGAAG 849
QY 281 AsnAsn 282
DB 850 AACAAAT 855
RESULT 10
AX491100 1204 bp DNA linear PAT 16-AUG-2002
LOCUS AX491100
DEFINITION Sequence 207 from Patent WO0200690.
ACCESSION AX491100
VERSION AX491100.1 GI:22323887
KEYWORDS
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITL Composition and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 207 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
SOURCE Location/Qualifiers
1..1204

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 306 a 364 c 294 g 240 t
ORIGIN
Alignment Scores:
Pred. No.: 6.64e-113 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-856-320A-2 (1-282) x AX491100 (1-1204)
QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
DB 10 ATGCAGAGGTGAGGTGGCTCGGGACTGGAAGTCATCGGCGACAGGCTCACAGACACC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
DB 70 AAGGAACCTGGGGCCCGCTCCCTCCAGGCCCATGAGGATTTCTGCACTTAATCTTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLysGlyPheGluCys 60
DB 130 CTTCCTGCGCAACAGGCTGTGAGGGGAGAGACAGGATCATCAAGGGGTGTGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluValThrArgLeuLeuGly 80
DB 190 AAGCCTCACTCCAGCCCTGGCAGAGACCCCTGTTCCAGAAAGACCGGCTACTCTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGCGCTCATGCCCCCAGATGGCTCTCGACAGAGCCCTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGlyGlnThrArgThr 120
DB 310 ATAGTTCACTGGGGCAGACCACTCCAGAAAGAGAGGGGTGTGAGACAGACCCGGACA 369
QY 121 SerThrSerSerProGlnLeuArgLeuProHisIleThrLeuArgCysAlaAsnIleThrIle 200
DB 430 AATGACATCATGCTGTGAAGATGGCATCGCATCTCCATCATCCTGGGCTGTGGACCC 489
QY 141 AsnAspIleMetLeuValIleMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 490 CTCACCTCTCTCTACCGCTGTGTCACTGTGACACAGCTGCTCATATTTCCGGCTGGGGC 549
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
DB 370 GCCACTGATCTCTCCCAACCCCGGCTTCAACACAGCCTCCCAACAAAGACCAACCGC 429
QY 181 SerThrSerSerProGlnLeuArgLeuProHisIleThrLeuArgCysAlaAsnIleThrIle 200
DB 550 AGCAGCTCAGGCCCGCCAGATGGCTCTGACACAGCCCTGCTCAACCCCGCTAC 609
QY 201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
DB 610 ATTGAGCACCGAAGTGTGAAGACCGCTACCCCGCAACATCACAGACACCATGATGTGT 669
QY 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
DB 670 GCCAGCGTCAGAGAGGGGGCAGAGACTCTCTGCAAGGTGACTCCGGGGGCCCTTGATC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB 730 TGTAACTGATCTCTTCAAGGCAATATCTCTGCGGCCAGAGTCTGTGCGATCAACCGA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLys 280
DB 790 AAGCTGTGTGTACACAAAGTGTGCAAAATATGTGACTGTGATCCAGAGACGATGAAG 849
QY 281 AsnAsn 282

Db 850 AACAA 855

RESULT 11
LOCUS AX697101 1204 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 169 from Patent WO0078961.
ACCESSION AX697101
KEYWORDS AX697101.1 GI:29498066
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 Ferrera, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnayers, L., Eaton, D.L., Gao, W.-Q., Pan, J., Botstein, D., Fong, S., Goddard, A., Godowski, P.J., Gutney, A.L., Smith, V., Tuma, D., Wood, W.I., Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K. Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0078961-A 169 28-DEC-2000;
Genentech Inc. (US)
FEATURES
source 1.1204
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 306 a 364 c 294 g 240 t
ORIGIN

Alignment Scores:
Pred. No.: 6,64e-113 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320A-2 (1-282) x AX697101 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db 10 ATGCAAGAGTTGAGTGGCTGGCGGAGCTGGAAGTATCGGGCAGAGCTTCACAGAGCC 69
QY 21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgLleLeuGlnLeuLleu 40
Db 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGCCATGAGATTCGAGTTAATCTTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgLleLeuGlyPheGlyLys 60
Db 130 CTTCCTCTGGCAACAGGCTTGTAGGGAGAGACCAAGATCATCAAGGGGTTCCAGTCC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuGly 80
Db 190 AAGCTTCACTCCAGCCCTGGCAGCAGCCCTGTTGAGAAGACGGGCTACTCTGTGG 249
QY 81 AlaThrLeuLleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db 250 GCGACCTCATCGCCCCCAGATGGCTCTGACAGCAGCCACAGCTCAAGCCCCCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlnGlnThrArgThr 120
Db 310 ATAGTTCACTGGGAGACACAACTCCAGAAAGAGAGAGGCTGTAGCAGACCCGAGCA 369
QY 121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db 370 GCCACTGAGTCTTCCCAACCCCGGCTTCAACCAAGCTCCCAACAAAGCAGCCGCC 429
QY 141 AsnAspLleMetLeuValLysMetAlaSerProValSerLleThrTrpAlaValArgPro 160
Db 430 AATGACATCATGCTGTGTGAAGATGATCGCCAGTCTCATCATCACTGGGCTGTGAGCC 489

QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLleSerGlyTrpGly 180
Db 490 CTCACCTCTCTCAACGCTGTGTCACTGTGGACACAGCTGCTATTTCGGGCTGGGCG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnLleThrLle 200
Db 550 AGCAGCTCCAGCCCCCAGTACGCTGCTCCACACCTTGCATGCGCCCAACATCACCAATC 609
QY 201 IleGluHisGlnLysCysGlnLeuAsnAlaTyrProGlyAsnLleThrAspThrMetValCys 220
Db 610 ATTGACACCAAGAGTGTAGAGACCGCTTACCCCGCAGATCATCAGACACCATGTGTGT 669
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyProLeuVal 240
Db 670 GCCAGGTCCAGAAAGGGGCAAGAGCTCTCCAGGGTGAATCCGGGGGCTCTGTGTC 729
QY 241 CysAsnGlnSerLeuGlnGlyLleLleSerTrpGlyGlnAspProCysAlaLleThrArg 260
Db 730 TGTAACTAGTCTTCAAGGCAATTAATCTCTGGGGCCAGGATCCGTGTGATCACCCGA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpLleGlnGlnThrLys 280
Db 790 AAGCTGTGTCTACACGAAAGTCTGCAATATGTGACTGGATCCAGAGACGATGAAG 849
QY 281 AsnAsn 282
Db 850 AACAA 855

RESULT 12
LOCUS BD091587 1301 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel serine protease BSSP6.
ACCESSION BD091587
VERSION BD091587.1 GI:22637198
KEYWORDS WO 0031257-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 1301)
Uemura, H., Okui, A., Komimami, K., Yamaguchi, N. and Mitsui, S. Novel serine protease BSSP6
Patent: WO 0031257-A 1 02-JUN-2000;
FUSO PHARMACEUTICAL INDUSTRIES LTD, HIDEOTOSHI UEMURA, AKIRA OKUI, KATSUYA KOMINAMI, NOZOMI YAMAGUCHI, SHINICHI MITSUI
COMMENT
OS Homo sapiens (human)
PN WO 0031257-A/1
PD 02-JUN-2000
PF 19-NOV-1999 WO 1999JP006476
PR 20-NOV-1998 JP 98P 347802
PI HIDEOTOSHI UEMURA, AKIRA OKUI, KATSUYA KOMINAMI, NOZOMI YAMAGUCHI, SHINICHI MITSUI
PC C12N15/12, C12N9/64, C12N5/06, C12N1/21, C07K16/40, C12P21/08, PC A01K67/027,
AO1K67/027,
CC G01N33/543
FH Key Location/Qualifiers.
FEATURES
source 1.1301
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 332 a 387 c 330 g 252 t
ORIGIN

Alignment Scores:
Pred. No.: 7,23e-113 Length: 1301
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320A-2 (1-282) x BD091587 (1-1301)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
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QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
 DB 173 AAGGAACCTGGGGCGGCTCTCCCGCCCTCCAGGCCATAGATTCTTGCAAGTTAACTCG 232

QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLeuGlyPheGlyCys 60
 DB 233 CTTCCTCTGGCAACAGGGCTTGTAGGGAGAGACCAAGATCATCAAGGGTTCCAGTGC 292

QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuGlyCys 80
 DB 293 AAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAGAGAGACGGGCTACTCTGTGG 352

QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 353 GCGACCCCTCATCGCCCGAGATGGCTCTGACAGCAGCCACCTGCTCAAGCCCGCTAC 412

QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGluGlyCysGluGlnThrArgThr 120
 DB 413 ATAGTTCACTGGGGGAGACACACCTCCAGAGAGAGAGGGCTGTAGCAGACCGGACA 472

QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 473 GCGACTGAGTCTCTCCCGACCCCGGCTTCAACAAACAGCTCCCAACAAAGACCAACCGC 532

QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 DB 533 AATGACATATCTGTGTAAGATGGCATGCCAGTCTTCATCATCAGCTGGGCTGTGGACCC 592

QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
 DB 593 CTCACCCCTCTCTCAGCTGTGTGCTGCTGGACACAGCTGCTCATTTCCGGCTGGGGC 652

QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 DB 653 ACACGCTCAGCCCGGAGTTAGCGCTGCTCAGACCTTCGATGGCCCAACATCACACATC 712

QY 201 IleGluHisGlnLysCysGlnLeuAlaIleTrpProGlyAsnIleThrAspThrMetValCys 220
 DB 713 ATTGAGCACAGAAAGTGAGAACCGCTACCCCGGCAACATCACAGACCATGTGTGT 772

QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
 DB 773 GCGAGCTGCAGAGAGGGGCAAGACCTCTGCGAGAGTACTCCGGGGCCCTCTGTGTC 832

QY 241 CysAsnGlnSerLeuGlnIleIleIleSerTrpGlyLysAspProCysAlaIleThrArg 260
 DB 833 TGTAAACCACTCTCTCAAGCATTAATCTCTGGGGCAGAGATCCGTTGTCATCACCGCA 892

QY 261 LysProGlyValIleThrLysValCysLysTyrValAspTrpIleGlnIleThrMetLys 280
 DB 893 AAGCCGTGGTCTACACGAAGCTGTCAATAATGTGACTGTGATCCAGAGAGCATGAG 952

QY 281 AsnAsn 282
 DB 953 AACCAT 958

RESULT 13
 AB041036 1301 bp mRNA linear PRI 20-JUN-2000
 LOCUS Homo sapiens mRNA for prostate-type hippostasin, complete cds.
 DEFINITION
 AB041036
 ACCESSION
 AB041036.1 GI:8574438
 VERSION
 AB041036.1
 KEYWORDS
 prostate-type hippostasin.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (sites)
 AUTHORS Mitsui,S., Yamada,T., Okui,A., Komimami,K., Uemura,H. and Yamaguchi,N.
 TITLE A novel isoform of a kallikrein-like protease, TUSP/hippostasin, (PRSS20), is expressed in the human brain and prostate
 JOURNAL Biochem. Biophys. Res. Commun. 272 (1), 205-211 (2000)
 MEDLINE 20329229
 PUBMED 10872828
 REFERENCE 2 (bases 1 to 1301)
 AUTHORS Yamaguchi,N. and Mitsui,S.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2000) Nozomi Yamaguchi, Kyoto Prefectural University of Medicine, Res. Ins. Geriatrics; Kawarachi Hirokoji, Kyoto, Kyoto 602-8566, Japan (E-mail:nozomi@koto.kpu-m.ac.jp, Tel:81-75-251-5848, Fax:81-75-251-5848)
 FEATURES
 source location/Qualifiers
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 /translation="MORLRMLRDWKSSGSGRLTAKEPGARSSPLQAMRLIQLILALATGLVGERIRIKFEKCPHSOPMOALFEKTRLCATLIPRLMLTAHCLKPRIVHLGQHNQKEREKSGOTRATSPSPHGGNSLPPKHDNDMLPKMSPVITVAARLTLSRCVTAGTSCILSGWSTSSPOLRIPLTPALCANITIIHOKCNAYAGNTIDTPMVCASVQSGKSDSCGSDSGPLVCQSLQGIISWQDPICATIRKGVITKCKYDWIOETMKNN"
 BASE COUNT 332 a 387 c 330 g 252 t
 ORIGIN

Alignment Scores:
 Pred. No.: 7,23e-113 Length: 1301
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-856-320A-2 (1-282) x AB041036 (1-1301)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
 DB 113 ATGCAAGAGTTGAGTGGCTGGCGGAGCTGGAAGTCATCGGGCAGAGGTCTCACAGACAGCC 172

QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
 DB 173 AAGGAACCTGGGGCGGCTCTCCCGCCCTCCAGGCCATAGATTCTTGCAAGTTAACTCG 232

QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLeuGlyPheGlyCys 60
 DB 233 CTTCCTCTGGCAACAGGGCTTGTAGGGAGAGACCAAGATCATCAAGGGTTCCAGTGC 292

QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuGlyCys 80
 DB 293 AAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAGAGAGACGGGCTACTCTGTGG 352

QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 353 GCGACCCCTCATCGCCCGAGATGGCTCTGACAGCAGCCACCTGCTCAAGCCCGCTAC 412

QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGluGlyCysGluGlnThrArgThr 120
 DB 413 ATAGTTCACTGGGGGAGACACACCTCCAGAGAGAGGGCTGTAGCAGACCGGACA 472

QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 473 GCGACTGAGTCTCTCCCGACCCCGGCTTCAACAAACAGCTCCCAACAAAGACCAACCGC 532

QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 Db 533 AATGACATCATGCTGTGAAGATGATGCATGCTCCATCATCCTGGGCTGTGGACCC 592
 QY 161 LeuThrLeuSerSerArgCysValIThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
 Db 593 CTCACCTCTCTCCAGCTGTGTCTGCTGTGGACAGCTGCTCTTCCTGGCTGGGCG 652
 QY 181 SerThrSerSerProGlnLeuArgLeuProIleThrLeuArgCysAlaSerIleThrIle 200
 Db 653 AGACATCCAGCCGCCAGTTAGCCTGCTCCATCAGCTTGGGATGCCCAACATCACCATC 712
 QY 201 IleGluHisGlnLysCysGluAsnAlaTyProGlyAsnIleThrAspThrMetValCys 220
 Db 713 ATTGACACACAGAAAGTGTGAAGAGCGCTACCCGGGCAACATCAGACACATGCTGT 772
 QY 221 AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
 Db 773 GCCAGCTGCAGAGAGGGGGCAAGAGACTCTGCGCAGGGTGACTCCGGGGGCTCTGCTC 832
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlnGlnAspProCysAlaIleThrArg 260
 Db 833 TGTAACTAGTCTCTTAAGGCAATTATCTCTGGGGCCAGGATCCGTGTGATCACCAG 892
 QY 261 LysProGlyValTyThrLysValCysLysTyValAspTrpIleGlnGlnThrMetLys 280
 Db 893 AAGCCGTGTCTACACGAAAGCTGCAATATGTGACTGCATCCAGAGAGCATGAAG 952
 QY 281 AsnAsn 282
 Db 953 AACAAAT 958

RESULT 14

AR098430
 LOCUS AR098430 1314 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 2 from patent US 6075136.
 ACCESSION AR098430
 VERSION AR098430.1 GI:12807687
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 AUTHORS Tang, Y. Tom, Corley, N.C. and Guegler, K.J.
 TITLE Prostate-associated serine protease
 JOURNAL Patent: US 6075136-A 2 13-JUN-2000;
 FEATURES
 source 1. 1314
 1. 1314
 /organism="unknown"

BASE COUNT 320 a 400 c 337 g 257 t
 ORIGIN

Alignment Scores:

Pred. No.: 7.31e-113 Length: 1314
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-856-320A-2 (1-282) x AR098430 (1-1314)

QY 1 MetGlnArgLeuValTrpLeuArgAspTrpLysSerSerGlyValArgGlyLeuThrAla 20
 Db 128 ATGCAAGAGGTGAAGGCTGCGGACTGGAAGTCAATCGGAGAGAGTCTCACAGACGC 187
 QY 21 LysGluProGlyAlaIleArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
 Db 188 AAGGAACCTGGGCGCCGCTCTCCCTCCAGGCATAGAGATTCTGAGATTAATCTCG 247
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLysGlyPheGlyCys 60
 Db 248 CTTGCTCTGGCAACAGGCTTGTAGGGGAGAGACAGATCATCAAGGGTTCCAGTGC 307

QY 61 LysProHisSerGlnProTrpGlnAlaIleLeuPheGluLysThrArgLeuLeuCysGly 80
 Db 308 AAGCTCTACTCCACAGCCCTGGCAGGACAGCCCTGTTGAGAAACCGCGCTACTCTGTGG 367
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTy 100
 Db 368 GCGAGCTCATGCGCCCGAGATGAGTCTCTGACAGAGCCCACTGCTCAAGCCCGCTAC 427
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120
 Db 428 ATAGTTCACTGGGGCAGACAACTCCAGAGAGAGAGGCTGTAGACAGACCCGAGACA 487
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 Db 488 GCCACTGAGTCTTCTCCCAAGCCCGCTTCAACAAAGCTTCCCAACAAAGACACCGC 547
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 Db 548 AATGACATCATGCTGTGAAGATGATGCATGCGCAGTCTCATCAGCTGGGCTGTGGACCC 607
 QY 161 LeuThrLeuSerSerArgCysValIThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
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 QY 181 SerThrSerSerProGlnLeuArgLeuProIleThrLeuArgCysAlaSerIleThrIle 200
 Db 668 AGCAGCTCCAGCCGCCAGTTAGCCTGCTCCATCAGCTTGGGATGCCCAACATCACCATC 727
 QY 201 IleGluHisGlnLysCysGluAsnAlaTyProGlyAsnIleThrAspThrMetValCys 220
 Db 728 ATTGACACACAGAAAGTGTGAAGAGCGCTACCCGGGCAACATCAGACACATGCTGT 787
 QY 221 AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
 Db 788 GCCAGCTGCAGAGAGGGGGCAAGAGACTCTGCGCAGGGTGACTCCGGGGGCTCTGCTC 847
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlnGlnAspProCysAlaIleThrArg 260
 Db 848 TGTAACTAGTCTCTTAAGGCAATTATCTCTGGGGCCAGGATCCGTGTGATCACCAG 907
 QY 261 LysProGlyValTyThrLysValCysLysTyValAspTrpIleGlnGlnThrMetLys 280
 Db 908 AAGCCGTGTCTACACGAAAGCTGCAATATGTGACTGCATCCAGAGAGCATGAAG 967
 QY 281 AsnAsn 282
 Db 968 AACAAAT 973

RESULT 15

BD130920
 LOCUS BD130920 1314 bp DNA linear PAT 18-SEP-2002
 DEFINITION Serine protease relating to human prostate.
 ACCESSION BD130920
 VERSION BD130920.1 GI:2325865
 KEYWORDS JP 2002503471-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Tang, T.Y., Corley, N.C. and Guegler, K.J.
 TITLE Serine protease relating to human prostate
 JOURNAL Patent: JP 2002503471-A 1 05-FEB-2002;
 COMMENT INCYTE PHARMACEUTICALS INC

OS Homo sapiens (human)
 PN JP 2002503471-A/1
 PD 05-FEB-2002
 PF 05-FEB-1999 JP 2000531566
 PR 17-FEB-1998 US 09/025059
 PI TOM Y TANG, NEIL C CORLEY, KARL J GUEGLER
 PC C07K16/40, A61K38/48, A61K45/00, A61P13/08, A61P15/00, A61P35/00,

PC C12N1/19,C12N1/21,C12N5/10,C12N9/64,C12Q1/68,C12N15/00,A61K37/
 PC 547,C12N5/00 Location/Qualifiers
 CC 2723646
 FH Key 1.1314
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 FT Location/Qualifiers
 1.1314
 /organism='Homo sapiens'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'

BASE COUNT 320 a 400 c 337 g 257 t
 ORIGIN

Alignment Scores:
 Pred. No.: 7.31e-113 Length: 1314
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-856-320A-2 (1-282) x BD130920 (1-1314)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAla 20
 DB 128 ATGCAGAGGTTGAGGGCTGGCGGACTGGAAGTCATCGGCAGAGGTTCCACAGAGCC 187
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
 DB 188 AAGGAACCTGGGGCCCGCTCTCTCCCTCCCGCCATGAGGATCTCGAGTTAATCTCG 247
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlyIleIleLysGlyPheGlyCys 60
 DB 248 CTTCCTCTGGCAACAGGCTTGTAGGGGAGAGACCAGATCATCAAGGGTTCCAGATCC 307
 QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyIleThrArgLeuLeuGly 80
 DB 308 AAGCTCATCTCCAGCCCTGGCAGGAGCCCTGTTGAGAAAGCGGCTACTCTGTGG 367
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 368 GCGAGCTCATGCCCCCGAGATGGCTCTCGACAGACGCCCACTGCTCAAGCCCCGTAC 427
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlnGlnThrArgThr 120
 DB 428 ATAGTTCACTGGGAGACCAACTCCGAGAGAGAGGCTGTGAGCAGACCCGAGACA 487
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 488 GCCACTGAATCTTCCCCCAGCCCGCTTCAACACAGCTCCCAACAAAGACCAACCGC 547
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 DB 548 AATGACATCATCTCTGTGAAGATGGCATGGCAGTCTCATCATCACTGGGCTGTGCAACC 607
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
 DB 608 CTCACCCCTCTCTCAAGCTGTGTCACTGTGGCACCAAGCTGCTCATTTCCGGCTGGGGC 667
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 DB 668 AGCAGCTCCAGCCCCCAGATTACGCTGTGCTCACACCTTGCGATGCGCCAAACATCACATC 727
 QY 201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
 DB 728 ATTGAGCACCAAGATGTGAGAACCGCTTACCCCGGCAACATCACAGACCACTGTGTGT 787
 QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyIleProLeuVal 240
 DB 788 GCCACGCTCCAGAGGGGCAAGGACTCTCTCCAGGGTGACTCCGGGGCCCTCTGGTC 847
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260

DB 848 TGTAACTGCTCTTCAAGGCATTATCTCTGGGGCCAGATCCGTGTGCATCACCCGA 907
 QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLys 280
 DB 908 AAGCTGTGTCTTACAGCAAGTCTGCAAAATATGTGACTGTGATCCAGGACGATGAAAG 967
 QY 281 AsnAsn 282
 DB 968 AACAAAT 973

Search completed: October 23, 2003, 18:05:15
 Job time : 4216.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 15:46:12 : Search time 41.9413 Seconds
(without alignments)
1067.227 Million cell updates/sec

Title: US-09-856-320a-2

Perfect score: 1523

Sequence: 1 MQRRLRLRLRWKSSGRGLTAA.....GVYTKCKYVDVIQETMKNN 282

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_19jun03.*

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22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1523	100.0	282	20	AAV42439
2	1523	100.0	282	21	AAAB11712
3	1523	100.0	282	21	AAV43636
4	1517	99.6	281	20	AAV42440
5	1355	89.0	250	21	AAAB21325
6	1355	89.0	250	21	AAV9390
7	1355	89.0	250	22	AAAB50479
8	1355	89.0	250	22	AAU12424
9	1355	89.0	250	22	AAAB6139

10	1355	89.0	250	23	ABG61816
11	1355	89.0	250	23	ABB95526
12	1355	89.0	250	23	ABBA4920
13	1355	89.0	250	23	AAU83684
14	1355	89.0	250	24	ABU66822
15	1355	89.0	250	24	ABU67098
16	1355	89.0	250	24	ABU59903
17	1355	89.0	250	24	ABU56739
18	1332.5	87.5	275	21	AAAB1714
19	1325	87.0	250	20	AAV36093
20	1324	86.9	248	22	AAE08017
21	1279.5	84.0	247	23	ABG70276
22	1252	82.2	228	21	AAAB21312
23	1237	80.6	289	21	AAAB36483
24	1227	80.6	289	22	AAAB67543
25	1187	77.9	276	21	AAAB1713
26	758	49.8	251	22	AAU16971
27	756	49.6	250	21	AAAB21298
28	756	49.6	250	23	ABP64969
29	754	49.5	247	22	AAU23217
30	748	49.1	246	20	AAW89041
31	748	49.1	246	22	ABAB5196
32	742.5	48.8	296	21	AAAB21297
33	736	48.3	247	22	AAU86677
34	736	48.3	247	22	AAU23752
35	736	48.3	247	22	AAU17043
36	698.5	45.9	260	17	AAW10694
37	698.5	45.9	260	18	AAW12393
38	698.5	45.9	260	23	ABAB5219
39	697	45.8	275	21	AAAB21311
40	696	45.7	320	23	AAE19166
41	696	45.7	320	23	AAU82732
42	692.5	45.5	256	23	AAU79390
43	690	45.3	260	20	AAV41744
44	690	45.3	260	20	AAV32852
45	690	45.3	260	20	AAV03220

ALIGNMENTS

RESULT 1	
ID	AAV42439
AAV42439	strand: Protein; 282 AA.
AAV42439;	
08-DEC-1999	(first entry)
CASB12	amino acid sequence.
neutropsin; cancer; assay; inhibitor; serine protease; immunogenic;	
autoimmune disease.	
Homo sapiens.	
WO9949055-A1.	
30-SEP-1999.	
17-MAR-1999;	99WO-EP01894.
20-MAR-1998;	98GB-0006095.
(SMK)	SMITHKLINE BEECHAM BIOLOGICALS.
Bruck CEM, Cassart J, Coche T, Vinals-bassols C;	
WPI. 1999-580450/49.	
N-PSDB; AA22638.	
New human serine protease CASB12, for treatment, prevention and	
diagnosis of cancer and autoimmune diseases	

XX Claim 3, Page 48, 58pp; English.

PS This is the amino acid sequence of the CASB12 protein. The nucleotide
 XX sequence of AA222638 shows homology with neuropilin and the encoded
 CC protein AA42439 is structurally related to other proteins of the
 CC serine protease family, having homology and/or structural similarity
 CC with neuropilin. It is expected that as well as similar structure, these
 CC proteins will also share similar biological functions and properties.
 CC The CASB12 polypeptides and polynucleotides can be used to develop
 CC methods for identifying agonists and antagonists/inhibitors of these
 CC molecules, and thereby treating conditions associated with CASB12
 CC polypeptide imbalance. The invention also provides for diagnostic assays
 CC for detecting diseases associated with inappropriate CASB12 polypeptide
 CC activity or levels.
 CC Since CASB12 is either specifically expressed or highly over-expressed
 CC in tumors compared to normal cells, the polypeptides and polynucleotides
 CC of the invention are believed to be important immunogens for specific
 CC prophylactic or therapeutic immunization against tumors. The
 CC polypeptides and polynucleotides can therefore be targeted by antigen
 CC specific immune reactions (which result in the destruction of the tumor
 CC cell) or they can be used to diagnose the occurrence of tumor cells

XX Sequence 282 AA;

Query Match 100.0%; Score 1523; DB 20; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.5e-134;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORLWRLRWKSSGGLTAKEPGARSSPLOAMRILOLLALATGLVGETRIIKGPEC 60
 Db 1 MORLWRLRWKSSGGLTAKEPGARSSPLOAMRILOLLALATGLVGETRIIKGPEC 60
 QY 61 KHSQPMQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHGOHMLQKEEGCEQRT 120
 Db 61 KHSQPMQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHGOHMLQKEEGCEQRT 120
 QY 121 ATESEFPHPGPNNSLPNKHNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCGISGWG 180
 Db 121 ATESEFPHPGPNNSLPNKHNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCGISGWG 180
 QY 181 STSSPOLRPLPHTLRCAANTITIEHOCENAYPGNITDTWVCASVOEGGKDCGDSGGPLV 240
 Db 181 STSSPOLRPLPHTLRCAANTITIEHOCENAYPGNITDTWVCASVOEGGKDCGDSGGPLV 240
 QY 241 CNOISLGIISWGQDPCATIRKPGVYTKVCKYVDWIOETMKN 282
 Db 241 CNOISLGIISWGQDPCATIRKPGVYTKVCKYVDWIOETMKN 282

RESULT 2
 AAB11712
 ID AAB11712 standard; Protein; 282 AA.

XX AAB11712;

XX 23-OCT-2000 (first entry)

XX Human serine protease BSSP6 (hbSSP6) SEQ ID NO:2.

XX BSSP6; serine protease; human; hbSSP6; mouse; mBSSP6; brain;
 KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
 KW epilepsy; cancer; inflammation; infertility; pancreatitis;
 KW prostatic hypertrophy.

XX Homo sapiens.

XX WO200031257-A1.

XX 02-JUN-2000.

XX 19-NOV-1999; 99WO-0P06476.

PR 20-NOV-1998; 98JP-0347802.

XX (FUSO) FUSO PHARM IND LTD.

XX Uemura H, Okui A, Komitani K, Yamaguchi N, Mitsui S;

XX WPI/2000-400067/34.

XX N-PSDB; AAA61763.

PT Serine protease BSSP6, useful in detecting homologs, mutants and
 PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
 PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
 PT using blood or other tissues

XX Claim 1; Page 69-70; 94pp; Japanese.

CC The invention relates to novel serine proteases designated BSSP6
 CC (AAB11712-B11714), and to nucleic acids encoding them (AAA61763-A61765).
 CC The invention also relates to vectors and transformants comprising BSSP6
 CC nucleic acids; transgenic animals in which the expression level of BSSP6
 CC can be varied; and an mBSSP6 knockout mouse. The invention additionally
 CC encompasses anti-BSSP6 antibodies and methods of production of such
 CC antibodies, methods of BSSP6 detection using the antibodies, and the
 CC use of BSSP6 proteins or fragments as diagnostic markers for certain
 CC medical conditions. Nucleotides encoding BSSP6 were initially
 CC isolated in a human brain cDNA library using degenerate PCR primers
 CC (AAA6195-A6196) based on conserved regions of serine proteases. The
 CC BSSP6 serine proteases and nucleotides encoding them are useful in
 CC detecting homologues, mutants and polymorphic variants in biological
 CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
 CC and spleen) as diagnostic markers for conditions such as Alzheimer's
 CC disease, epilepsy, cancer, inflammation, infertility and prostatic
 CC hypertrophy. Sequences AAB11712 and AAB11714 represent human BSSP6
 CC variants (hbSSP6), and sequence AAB11713 represents murine BSSP6
 CC (mBSSP6).

XX Sequence 282 AA;

Query Match 100.0%; Score 1523; DB 21; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.5e-134;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORLWRLDWKSSGGLTAKEPGARSSPLOAMRILOLLALATGLVGETRIIKGPEC 60

Db 1 MORLWRLDWKSSGGLTAKEPGARSSPLOAMRILOLLALATGLVGETRIIKGPEC 60

QY 61 KHSQPMQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHGOHMLQKEEGCEQRT 120

Db 61 KHSQPMQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHGOHMLQKEEGCEQRT 120

QY 121 ATESEFPHPGPNNSLPNKHNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCGISGWG 180

Db 121 ATESEFPHPGPNNSLPNKHNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCGISGWG 180

QY 181 STSSPOLRPLPHTLRCAANTITIEHOCENAYPGNITDTWVCASVOEGGKDCGDSGGPLV 240

Db 181 STSSPOLRPLPHTLRCAANTITIEHOCENAYPGNITDTWVCASVOEGGKDCGDSGGPLV 240

QY 241 CNOISLGIISWGQDPCATIRKPGVYTKVCKYVDWIOETMKN 282

Db 241 CNOISLGIISWGQDPCATIRKPGVYTKVCKYVDWIOETMKN 282

RESULT 3

XX AA43636
 ID AA43636 standard; Protein; 282 AA.

XX AA43636;

XX 11-FEB-2000 (first entry)

XX A human prostate-associated serum protease (PRASP).

KW Human; prostate-associated serum protease; PRASP; neuropsin; PSA;
 KW Incyte clone 2723646; reproductive disorder; cancer;
 KW abnormal prolactin production; infertility; tubal disease;
 KW ovulatory defect; endometriosis; polycystic ovary syndrome;
 KW autoimmune disorder; ectopic pregnancy; breast cancer;
 KW abnormal spermatogenesis; testicular cancer; adenocarcinoma; leukaemia;
 KW lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..50 /note= "signal sequence"
 FT Modified-site 13 /note= "potential protein kinase C phosphorylation site"
 FT Disulfide-bond 60 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Disulfide-bond 79 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Active-site 90..95 /note= "serine protease trypsin family active site motif"
 FT Misc-difference 94 /note= "this forms the active site catalytic triad with Asp142 and Ser235"
 FT Disulfide-bond 95 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 120 /note= "potential casein kinase II phosphorylation site"
 FT Modified-site 131 /note= "potential N-glycosylation site"
 FT Misc-difference 142 /note= "this forms the active site catalytic triad with His94 and Ser235"
 FT Modified-site 164 /note= "potential protein kinase C phosphorylation site"
 FT Disulfide-bond 174 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 192 /note= "potential protein kinase C phosphorylation site"
 FT Disulfide-bond 195 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 197 /note= "potential N-glycosylation site"
 FT Modified-site 199 /note= "potential casein kinase II phosphorylation site"
 FT Disulfide-bond 206 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 213 /note= "potential N-glycosylation site"
 FT Disulfide-bond 220 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 222 /note= "potential casein kinase II phosphorylation site"
 FT Active-site 229..240 /note= "serine protease trypsin family active site motif"
 FT Misc-difference 229 /note= "the corresponding residue (together with Ser235, Gly252 and Gly263) in neuropsin forms a oxyanion hole"

FT Disulfide-bond 231 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Misc-difference 235 /note= "the corresponding residue (together with Asp229, Gly252 and Gly263) in neuropsin forms a oxyanion hole"
 FT Misc-difference 235 /note= "this forms the active site catalytic triad with His94 and Asp142"
 FT Disulfide-bond 241 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 242 /note= "potential N-glycosylation site"
 FT Misc-difference 252 /note= "the corresponding residue (together with Asp229, Ser235 and Gly263) in neuropsin forms a oxyanion hole"
 FT Disulfide-bond 256 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 259 /note= "potential protein kinase C phosphorylation site"
 FT Misc-difference 263 /note= "the corresponding residue (together with Asp229, Ser235 and Gly252) in neuropsin forms a oxyanion hole"
 FT Modified-site 278 /note= "potential protein kinase C phosphorylation site"
 XX
 XX WO9941387-A2.
 XX 19-AUG-1999.
 XX 05-FEB-1999; 99WO-US02571.
 XX 17-FEB-1998; 98US-0025059.
 XX (INCY-) INCYTE PHARM INC.
 PI Tang YT, Corley NC, Guegler KJ;
 DR WPI; 2000-012993/01.
 DR N-PSDB; AA230222.
 PT New prostate-associated serum protease and polynucleotides which identify and encode PRASP, useful for treating reproductive disorders and cancer
 XX
 XX Claim 1; Fig 1A-D; 67pp; English.
 PS
 CC The present sequence represents human prostate-associated serum protease (PRASP). The protein shows homology to neuropsin, a brain-specific protease in mice, and PSA, a prostate-specific protease in humans.
 CC Nucleic acids encoding PRASP were first identified in Incyte clone 2723646 from the lung tumour cDNA library. Pharmaceutical compositions containing PRASP, or antibodies to PRASP, and mimetics, agonists, antagonists or inhibitors of PRASP, are used for treating or preventing a reproductive disorder or cancer. Examples of reproductive disorder include, abnormal prolactin production, infertility, tubal disease, ovulatory defects, endometriosis, polycystic ovary syndrome, autoimmune disorders, ectopic pregnancy, breast cancer, abnormal spermatogenesis and testicular cancer. Examples of cancers which may be treated or prevented include adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid and uterus. A vector capable of expressing PRASP or an agonist which modulates the activity of PRASP may be administered to treat or prevent a reproductive disorder or

```
CC cancer.
XX
SQ Sequence 282 AA:
Query Match 100.0%; Score 1523; DB 21; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.5e-134;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORLRMLRWKSSGRLTAKEPGARSSPLQAMRIQLILALATGLVGGERRIIKGFEC 60
DB 1 MORLRMLRWKSSGRLTAKEPGARSSPLQAMRIQLILALATGLVGGERRIIKGFEC 60
QY 61 KPHSQPMQALFEKTRILCGATILAPRWLLTAHCLKPRYIVHIGQHNLOKEEGCEQRT 120
DB 61 KPHSQPMQALFEKTRILCGATILAPRWLLTAHCLKPRYIVHIGQHNLOKEEGCEQRT 120
QY 121 ATESEFPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPTLSRCVTAGTSCGISG 180
DB 121 ATESEFPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPTLSRCVTAGTSCGISG 180
QY 181 STSSPOLRLPHTLRCAANTITIIHOKCENAYPGNITDTWVCASVQEGKDCSGDSG 240
DB 181 STSSPOLRLPHTLRCAANTITIIHOKCENAYPGNITDTWVCASVQEGKDCSGDSG 240
QY 241 CNOSLOGIISWGODPCATIRKPGVYTKVCKYVDMIOETMKN 282
DB 241 CNOSLOGIISWGODPCATIRKPGVYTKVCKYVDMIOETMKN 282

RESULT 4
AAV42440
ID AAV42440 standard; Protein; 281 AA.
AC AAV42440;
DT 08-DEC-1999 (first entry)
DE CASB12 polypeptide derived from Expressed Sequence Tag products.
XX neurospain; cancer; assay; inhibitor; serine protease; immunogenic;
XX autoimmune disease.
XX Homo sapiens.
OS WO9949055-A1.
PN 30-SEP-1999.
XX 17-MAR-1999; 99WO-EP01894.
XX 20-MAR-1998; 98GB-0006095.
XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PA
XX Bruck CEM, Cassart J, Coche T, Vinals-bassols C;
XX WPI; 1999-580450/49.
XX N-PSDB; AA22639.
XX New human serine protease CASB12, for treatment, prevention and
XX diagnosis of cancer and autoimmune diseases
XX Claim 27; Page 49-50; 58pp; English.
XX
XX This is the amino acid sequence of CASB12 protein, derived from an
XX Expressed Sequence Tag (EST) search for tumor-specific and
XX tumor-associated antigens. The nucleotide sequence of AA22638 shows
XX homology with neurospain and the encoded protein AAV42439 is structurally
XX related to other proteins of the serine protease family, having homology
XX and/or structural similarity with neurospain. It is expected that as well
XX as similar structure, these proteins will also share similar biological
XX functions and properties.
XX The CASB12 polypeptides and polynucleotides can be used to develop
```

```
CC methods for identifying agonists and antagonists/inhibitors of these
CC molecules, and thereby creating conditions associated with CASB12
CC polypeptide imbalance. The invention also provides for diagnostic assays
CC for detecting diseases associated with inappropriate CASB12 polypeptide
CC activity or levels.
CC Since CASB12 is either specifically expressed or highly over-expressed
CC in tumors compared to normal cells, the polypeptides and polynucleotides
CC of the invention are believed to be important immunogens for specific
CC prophylactic or therapeutic immunization against tumors. The
CC polypeptides and polynucleotides can therefore be targeted by antigen
CC specific immune reactions (which result in the destruction of the tumor
CC cell) or they can be used to diagnose the occurrence of tumor cells

SQ Sequence 281 AA:
Query Match 99.6%; Score 1517; DB 20; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-134;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORLRMLRWKSSGRLTAKEPGARSSPLQAMRIQLILALATGLVGGERRIIKGFEC 60
DB 1 MORLRMLRWKSSGRLTAKEPGARSSPLQAMRIQLILALATGLVGGERRIIKGFEC 60
QY 61 KPHSQPMQALFEKTRILCGATILAPRWLLTAHCLKPRYIVHIGQHNLOKEEGCEQRT 120
DB 61 KPHSQPMQALFEKTRILCGATILAPRWLLTAHCLKPRYIVHIGQHNLOKEEGCEQRT 120
QY 121 ATESEFPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPTLSRCVTAGTSCGISG 180
DB 121 ATESEFPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPTLSRCVTAGTSCGISG 180
QY 181 STSSPOLRLPHTLRCAANTITIIHOKCENAYPGNITDTWVCASVQEGKDCSGDSG 240
DB 181 STSSPOLRLPHTLRCAANTITIIHOKCENAYPGNITDTWVCASVQEGKDCSGDSG 240
QY 241 CNOSLOGIISWGODPCATIRKPGVYTKVCKYVDMIOETMKN 281
DB 241 CNOSLOGIISWGODPCATIRKPGVYTKVCKYVDMIOETMKN 281

RESULT 5
AAB21325
ID AAB21325 standard; Protein; 250 AA.
AC AAB21325;
DT 02-FEB-2001 (first entry)
DE Human TLSP.
XX
XX Human; KUK-L1; KUK-L2; KUK-L3; KUK-L4; KUK-L5; KUK-L6; TLSP;
XX trypsin-like serine protease; kallikrein-like protein; serine protease;
XX cytosolic; cancer; prostrate cancer.
XX
XX Homo sapiens.
OS WO200053776-A2.
PN 14-SEP-2000.
XX 09-MAR-2000; 2000WO-CA00258.
XX 11-MAR-1999; 99US-0124260.
XX 01-APR-1999; 99US-0127386.
XX 21-JUL-1999; 99US-0144919.
XX (MOUN ) MOUNT SINAI HOSPITAL.
XX PA
XX Yousef GM, Diamandis EP;
XX WPI; 2000-587440/55.
XX New kallikrein-like (KUK-L) proteins for diagnosing and treating KUK-L
```

PT protein mediated disorders, especially cancer. -
XX Example 5; Fig 27; 184p; English.
PS
XX
CC The present sequence is human trypsin-like serine protease (TLSP), a
CC member of the serine protease family. Kallikreins and
CC kallikrein-like proteins are a subgroup of the serine protease enzyme
CC family. They catalyze the selective cleavage of specific polypeptide
CC precursors to release peptides with potent biological activity. Nucleic
CC acids encoding kallikrein-like proteins KLK-11, KLK-12, KLK-13, KLK-14,
CC KLK-15 and KLK-16 have been isolated. The proteins are useful in the
CC treatment, monitoring and diagnosis of cancers, especially prostate
CC cancer. They can also be used to identify a substance that can associate
CC with or mediate the biological activity of the proteins. Antibodies can
CC be used to treat conditions mediated by the kallikrein-like proteins.
XX
SQ Sequence 250 AA;
Query Match 89.0%; Score 1355; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.6e-119;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 MHLIQLILALATGLVGETRIIKGFECRPHSQPMQALFETRLICGATLIAPRWLTA 92
DB 1 MHLIQLILALATGLVGETRIIKGFECRPHSQPMQALFETRLICGATLIAPRWLTA 60
QY 93 AHCLPRYIVHLGQHNLOKEGCEQRTATSESPHPGPNNSLPNDHRNDILVMASPV 152
DB 61 AHCLPRYIVHLGQHNLOKEGCEQRTATSESPHPGPNNSLPNDHRNDILVMASPV 120
QY 153 SITMAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRLPHTLRCAITIIIEHOKENAVPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRLPHTLRCAITIIIEHOKENAVPG 180
QY 213 NITDMVACASVQEGKDCSQGSGPLVNCQSLGIIISGQDPCAITRKPGYITVCKXV 272
DB 181 NITDMVACASVQEGKDCSQGSGPLVNCQSLGIIISGQDPCAITRKPGYITVCKXV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250
RESULT 6
AA99390
ID AA99390 standard; Protein; 250 AA.
XX
AC AA99390;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1279 (UNO649) amino acid sequence SEQ ID NO:170.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
FN WO200012708-A2.
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20111.
XX
PR 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.

PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099816.
PR 10-SEP-1998; 98US-0099815.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101016.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101744.
PR 24-SEP-1998; 98US-0101745.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 30-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103259.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103335.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104287.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.

CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 CC anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimer's; vascular;
 CC antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. similar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA3185 to
 CC ABA3193 and ABA50300 represent sequences used in the exemplification of
 CC the present invention.

XX Sequence 250 AA;

Query Match 89.0%; Score 1355; DB 22; Length 250;

Best Local Similarity 100.0%; Pred. No. 7, 6e-119; Indels 0; Gaps 0;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRILQILALATGIVGSETRIIKGFCKPHSPQWQALFEKTRLLCGATLIAPRWLTA 92
 DB 1 MRILQILALATGIVGSETRIIKGFCKPHSPQWQALFEKTRLLCGATLIAPRWLTA 60
 QY 93 AHCLKPRYIVHGOHNLQKEGCEQTRTATESFPHPGFNNSLPNKHNDIMLVKMASPV 152
 DB 61 AHCLKPRYIVHGOHNLQKEGCEQTRTATESFPHPGFNNSLPNKHNDIMLVKMASPV 120
 QY 153 SITWAVRPLTSSRCVTAGTSCILSGWGSTSSPOLRPLPTLRCANTITIEHOKCENAYPG 212
 DB 121 SITWAVRPLTSSRCVTAGTSCILSGWGSTSSPOLRPLPTLRCANTITIEHOKCENAYPG 180
 QY 213 NITDINVCASVQEGKDSQGDSPGLVNCGLGIIISWGQPCAITRRPGVYTRCKXV 272
 DB 181 NITDINVCASVQEGKDSQGDSPGLVNCGLGIIISWGQPCAITRRPGVYTRCKXV 240

RESULT 8

AAU12424 standard; Protein; 250 AA.

AAU12424;

24-OCT-2001 (first entry)

Human PRO1279 polypeptide sequence.

Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 breast; prostate; cervical; tumour necrosis factor- α ; TNF- α ; TNF- α ;
 cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 adipocyte; A-peptide; factor VIIA; gene therapy.

Homo sapiens.

WO200140466-A2.

07-JUN-2001.

01-DEC-2000; 2000WO-US32678.

01-DEC-1999; 99WO-US28301.

01-DEC-1999; 99WO-US28634.

02-DEC-1999; 99WO-US28551.

02-DEC-1999; 99WO-US28564.

09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.

(GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
 Gerilsen ME, Goddard A, Godowski PJ, Gurney AU, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;

WPI, 2001-408281/43.

N-PSDB; AAS21496.

Isolated, secretory and transmembrane PRO polypeptide used to detect
 other PRO polypeptides, link bioactive molecules to cells expressing
 PRO polypeptides, and detect the presence of mammalian tumours e.g.
 lung, breast, prostate, cervical

Claim 12; Fig 506; 813pp; English.

AAU12172-AAU12446 represent novel human secretory and transmembrane
 PRO polypeptides. The PRO polypeptides are useful to detect other
 PRO polypeptides, to link bioactive molecules to cells expressing
 PRO polypeptides, to modulate biological activities of cells expressing
 PRO polypeptides, and to detect the presence of mammalian lung, colon,
 breast, prostate, rectal, cervical or liver tumours by comparing PRO
 polypeptide expression in a cell sample to that in a control sample.
 Some of the 275 sequences are also useful to stimulate the release of
 tumour necrosis factor- α (TNF- α) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.

Sequence 250 AA;

Query Match 89.0%; Score 1355; DB 22; Length 250;

Best Local Similarity 100.0%; Pred. No. 7, 6e-119; Indels 0; Gaps 0;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRILQILALATGIVGSETRIIKGFCKPHSPQWQALFEKTRLLCGATLIAPRWLTA 92

DB 1 MRILQILALATGIVGSETRIIKGFCKPHSPQWQALFEKTRLLCGATLIAPRWLTA 60

QY 93 AHCLKPRYIVHGOHNLQKEGCEQTRTATESFPHPGFNNSLPNKHNDIMLVKMASPV 152

DB 61 AHCLKPRYIVHGOHNLQKEGCEQTRTATESFPHPGFNNSLPNKHNDIMLVKMASPV 120

QY 153 SITMAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRLPHTLRCAANTITIEHOKENAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRLPHTLRCAANTITIEHOKENAYPG 180
QY 213 NITDTMVCASVOEGKDSQCGDSGGLVNCNOSLOGIISWGDDPCAITRKPQVYTKVKCV 272
DB 181 NITDTMVCASVOEGKDSQCGDSGGLVNCNOSLOGIISWGDDPCAITRKPQVYTKVKCV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250
RESULT 9
ID AAB66139 standard; protein; 250 AA.
AC AAB66139;
XX
XX
DT 02-APR-2001 (first entry)
DE Protein of the invention #51.
XX
KW Secreted; transmembrane; gene therapy.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US04342.
XX
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 16-DEC-1999; 99WO-US30095.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
XX
XX (GETH) GENENTECH INC.
PA
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Piont NF, Roy MA, Smith V, Stewart TA, Tumas D;
PI Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy -
XX
PS Claim 1; Fig 102; 787bp; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of
CC anti-sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents.
CC The nucleic acids may also be used in gene therapy.
XX
XX Sequence 250 AA;
SQ
Query Match 89.0%; Score 1355; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 7,66-119;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLIOLILALATGIVGETRIIIGFEEKPHSOPMOALLFEKTRLLCGATLIAPRWLLTA 92
DB 1 MRLIOLILALATGIVGETRIIIGFEEKPHSOPMOALLFEKTRLLCGATLIAPRWLLTA 60
QY 93 AHLCKPRYIVHAGHNLQKEGCEQOTRTATSSFPHPFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHLCKPRYIVHAGHNLQKEGCEQOTRTATSSFPHPFNNSLPNKDHRNDIMLVKMASPV 120
QY 153 SITMAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRLPHTLRCAANTITIEHOKENAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRLPHTLRCAANTITIEHOKENAYPG 180
QY 213 NITDTMVCASVOEGKDSQCGDSGGLVNCNOSLOGIISWGDDPCAITRKPQVYTKVKCV 272
DB 181 NITDTMVCASVOEGKDSQCGDSGGLVNCNOSLOGIISWGDDPCAITRKPQVYTKVKCV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250
RESULT 10
ID ABG61816 standard; Protein; 250 AA.
AC ABG61816;
XX
XX
DT 15-AUG-2002 (first entry)
DE Prostate cancer-associated protein #17.
XX
XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
XX
XX Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US32045.
XX
PR 13-OCT-2000; 2000US-0687576.
PR 08-DEC-2000; 2000US-0733288.
PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276791P.
PR 16-MAR-2001; 2001US-276888P.
PR 06-APR-2001; 2001US-281922P.
PR 24-APR-2001; 2001US-286214P.
PR 30-APR-2001; 2001US-0847046.
PR 04-MAY-2001; 2001US-288589P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
PA
PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
XX WPI; 2002-471335/50.
XX
XX N-PSDB; ABK92131.
XX
XX Detecting a prostate cancer-associated transcript in a cell in a
PT patient, useful for diagnosing prostate cancer (PC) or screening
PT modulators of PC, by determining if prostate cancer-associated genes
XX are expressed in a prostate tissue -
XX
PS Claim 27; Page 314; 436bp; English.
XX
XX The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridise to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in

CC prostate cancer and are derived from the tissues of various
 CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
 CC The methods of the invention are useful for diagnosing and treating
 CC prostate cancer in mammals. The prostate cancer-associated genes are
 CC useful for diagnosing or treating prostate cancer, as well as for
 CC identifying modulators of prostate cancer or agents that inhibit
 CC prostate cancer. The nucleic acid sequences are particularly useful
 CC in gene therapy, as a vaccine or in antisense applications.
 CC ABG61800-ABG61944 represent prostate cancer-associated proteins.

XX Sequence 250 AA:

Query Match 89.0%; Score 1355; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 7.6e-119;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLQLILALATGVLGGETRIIKGFECRPHSQPQALFEKTRLLCGATLIAPRWLTA 92
 DB 1 MRLQLILALATGVLGGETRIIKGFECRPHSQPQALFEKTRLLCGATLIAPRWLTA 60
 QY 93 AHCLKRXYIVHGOHNLQKEGCEQRTATSESPHGFNNSLPNKDRNDIMLVKASPV 152
 DB 61 AHCLKRXYIVHGOHNLQKEGCEQRTATSESPHGFNNSLPNKDRNDIMLVKASPV 120
 QY 153 SITWAVRPLTSSRCYTAGTSCILISGSGTSSPOLRPHTLRCANITIIHOKCENAYPG 212
 DB 121 SITWAVRPLTSSRCYTAGTSCILISGSGTSSPOLRPHTLRCANITIIHOKCENAYPG 180
 QY 213 NITDTWVCASVQEGKDCQSGDSGSPVLCNOSIQIISWGDPICATRRKPYVTKXKV 272
 DB 181 NITDTWVCASVQEGKDCQSGDSGSPVLCNOSIQIISWGDPICATRRKPYVTKXKV 240
 QY 273 DWIOETMKNN 282
 DB 241 DWIOETMKNN 250

RESULT 11

AB955526
 ID ABB95526 standard; Protein; 250 AA.

XX ABB95526;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
 XX
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiac; cytoskeletal; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US21735.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 28-JUL-2000; 2000US-220664P.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23322.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 24-OCT-2000; 2000US-242922P.
 PR

PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806889.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.

PA (GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRTSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODOWSKI P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANJ) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.

PI Baker KP, Ferrara N, Gerber H, Gerttsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 DR WPI; 2002-171999/22.
 DR N-PSDB; ABL95664.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -

Claim 11; Fig 208; 567pp; English.

XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angioneuroma, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 250 AA:

Query Match 89.0%; Score 1355; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 7.6e-119;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLQLILALATGVLGGETRIIKGFECRPHSQPQALFEKTRLLCGATLIAPRWLTA 92
 DB 1 MRLQLILALATGVLGGETRIIKGFECRPHSQPQALFEKTRLLCGATLIAPRWLTA 60

```

QY 93 AHCLKPRYIVHLGQHNLOKEBCEQOTRTATSFPHPGFNNSLPNKDHRNDIMLVKMA SPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEBCEQOTRTATSFPHPGFNNSLPNKDHRNDIMLVKMA SPV 120
QY 153 SITWAVRPLTSSRCVTAGTSCLSISGWGTSSTSPOLRPLPHTLRCA NITIIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCLSISGWGTSSTSPOLRPLPHTLRCA NITIIIEHOKCENAYPG 180
QY 213 NITDTMVCASVQEGKSCQGDGSGPLVCNOSLOGIISWGDPCAITRKPGVYTKVCKV 272
DB 181 NITDTMVCASVQEGKSCQGDGSGPLVCNOSLOGIISWGDPCAITRKPGVYTKVCKV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

RESULT 12
AB84920
ID AB84920 standard; Protein; 250 AA.
XX
AC AB84920;
XX
DE 16-MAY-2002 (first entry)
XX
XX Human PRO1279 protein sequence SEQ ID NO:208.
XX
KW Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
XX 20-JUN-2001; 2001WO-US19692.
XX
XX 23-JUN-2000; 2000US-213637P.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222695P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US23522.
XX 07-SEP-2000; 2000US-230978P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242922P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-MAR-2001; 2001WO-US06666.
XX 09-MAR-2001; 2001US-0802706.
XX 14-MAR-2001; 2001US-0808689.
XX 22-MAR-2001; 2001US-0816744.
XX 05-APR-2001; 2001US-0828366.
XX 10-MAY-2001; 2001US-0854208.

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PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gertlsten ME, Goddard A,
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
XX Stephan WF, Watanabe CK, Williams FW, Wood WI, Ye W,
XX WPI; 2002-090516/12.
XX N-PSDB; ABL88175.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 208; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,
XX antiangiogenic, hypotensive, vulnerability and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX in molecular biology, including use as hybridisation probes, and in
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX probes used in the exemplification of the present invention.
XX
XX SQ Sequence 250 AA;
XX
XX Query Match 89.0%; Score 1355; DB 23; Length 250;
XX Best Local Similarity 100.0%; Pred. No. 7,6e-119;
XX Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 33 MRLIQLILALATGLVGETRIIKGFECCKPHSQPQAALEFKTRLGATLIAPRWLITA 92
DB 1 MRLIQLILALATGLVGETRIIKGFECCKPHSQPQAALEFKTRLGATLIAPRWLITA 60
QY 93 AHCLKPRYIVHLGQHNLOKEBCEQOTRTATSFPHPGFNNSLPNKDHRNDIMLVKMA SPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEBCEQOTRTATSFPHPGFNNSLPNKDHRNDIMLVKMA SPV 120
QY 153 SITWAVRPLTSSRCVTAGTSCLSISGWGTSSTSPOLRPLPHTLRCA NITIIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCLSISGWGTSSTSPOLRPLPHTLRCA NITIIIEHOKCENAYPG 180
QY 213 NITDTMVCASVQEGKSCQGDGSGPLVCNOSLOGIISWGDPCAITRKPGVYTKVCKV 272
DB 181 NITDTMVCASVQEGKSCQGDGSGPLVCNOSLOGIISWGDPCAITRKPGVYTKVCKV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

RESULT 13
AAU83684
ID AAU83684 standard; Protein; 250 AA.
XX
AC AAU83684;
XX
XX 08-MAY-2002 (first entry)
XX

```

DE Human PRO protein, Seq ID No 186.
 XX
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 XX tumour necrosis factor-alpha.
 OS Homo sapiens.
 XX
 XX WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 XX 29-JUN-2001; 2001WO-US21066.
 XX
 XX 20-JUL-2000; 2000US-219556P.
 XX 25-JUL-2000; 2000US-220585P.
 XX 25-JUL-2000; 2000US-220605P.
 XX 25-JUL-2000; 2000US-220607P.
 XX 25-JUL-2000; 2000US-220624P.
 XX 25-JUL-2000; 2000US-220638P.
 XX 25-JUL-2000; 2000US-220664P.
 XX 25-JUL-2000; 2000US-220666P.
 XX 26-JUL-2000; 2000US-220833P.
 XX 28-JUL-2000; 2000WO-US20710.
 XX 23-AUG-2000; 2000WO-US23328.
 XX 24-AUG-2000; 2000WO-US23328.
 XX 15-SEP-2000; 2000WO-US0000P.
 XX 10-NOV-2000; 2000WO-US30873.
 XX 28-NOV-2000; 2000US-253646P.
 XX 01-DEC-2000; 2000WO-US32678.
 XX 20-DEC-2000; 2000US-0747259.
 XX 28-FEB-2001; 2001WO-US06520.
 XX 10-MAY-2001; 2001US-0854280.
 XX 25-MAY-2001; 2001WO-US17092.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
 XX
 DR WPI; 2002-172001/22.
 DR N-PSDB; ABR33628.
 XX
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 XX
 XX Claim 11; Figure 186; 359pp; English.
 XX
 XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AUB3592-AAUB3713 represent human PRO
 CC protein sequences of the invention.
 XX
 XX Sequence 250 AA:
 XX
 XX Query Match 89.0%; Score 1355; DB 23; Length 250;
 XX Best Local Similarity 100.0%; Pred. No. 7.6e-119;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 MRLILILILALATGIVGETRIIKGPECKPHSPQMAALFETRLICGATLLAPRWLLTA 92
 Db 1 NRIILILILALATGIVGETRIIKGPECKPHSPQMAALFETRLICGATLLAPRWLLTA 60
 QY 93 AHCLKPRYIVHLGQHNLOKEBCEQTRTATESFPHPGFNNSLPNDRNDIMLVKMASPV 152
 Db 61 AHCLKPRYIVHLGQHNLOKEBCEQTRTATESFPHPGFNNSLPNDRNDIMLVKMASPV 120
 QY 153 SITMAVRPLTSSRCVTAAGTSCGISGWSSTSPQLRLPHTLRCAINITIIEHCKENAYPG 212
 Db 121 SITMAVRPLTSSRCVTAAGTSCGISGWSSTSPQLRLPHTLRCAINITIIEHCKENAYPG 180
 QY 213 NITDTMVCASVOEGGKSCQGDGSPVLCNOSLOGIISMGDPICATIRKPGVYTVCKVY 272
 Db 181 NITDTMVCASVOEGGKSCQGDGSPVLCNOSLOGIISMGDPICATIRKPGVYTVCKVY 240
 QY 273 DWIOETMKNN 282
 Db 241 DWIOETMKNN 250
 RESULT 14
 AUB66822
 ID AUB66822 standard; Protein; 250 AA.
 XX
 AC AUB66822;
 XX
 DT 23-MAY-2003 (first entry)
 XX
 XX Human PRO polypeptide #253.
 DE
 XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KW differentiation; chondrocyte; tumour; genetic disorder;
 KW cytosolic.
 XX
 XX OS Homo sapiens.
 XX
 XX US2003036180-A1.
 XX
 PD 20-FEB-2003.
 XX
 XX
 PF 09-MAY-2002; 2002US-0143114.
 XX
 XX 31-MAR-1997; 97WO-US05230.
 XX 12-JUN-1998; 98WO-US12456.
 XX 14-JUL-1998; 98WO-US14552.
 XX 28-AUG-1998; 98WO-US17888.
 XX 10-SEP-1998; 98WO-US18824.
 XX 14-SEP-1998; 98WO-US19093.
 XX 14-SEP-1998; 98WO-US19094.
 XX 16-SEP-1998; 98WO-US19177.
 XX 17-SEP-1998; 98WO-US19330.
 XX 07-OCT-1998; 98WO-US19437.
 XX 29-OCT-1998; 98WO-US21141.
 XX 29-OCT-1998; 98WO-US22991.
 XX 20-NOV-1998; 98WO-US24855.
 XX 01-DEC-1998; 98WO-US25108.
 XX 05-JAN-1999; 99WO-US00106.
 XX 08-MAR-1999; 99WO-US05028.
 XX 10-MAR-1999; 99WO-US05190.
 XX 20-APR-1999; 99WO-US08615.
 XX 14-MAY-1999; 99WO-US10733.
 XX 02-JUN-1999; 99WO-US12252.
 XX 01-SEP-1999; 99WO-US20111.
 XX 08-SEP-1999; 99WO-US20594.
 XX 13-SEP-1999; 99WO-US20944.
 XX 15-SEP-1999; 99WO-US21090.
 XX 05-OCT-1999; 99WO-US21547.
 XX 99WO-US23089.

PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28501.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 22-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US15941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX

PA (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR MPI: 2003-332040/31.
 DR N-PSDB; ACD03855.
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification -
 XX
 PS Claim 12; Fig 506; 660pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. ABU6570-ABU6684 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/patseq/idententry.html.
 XX
 SQ Sequence 250 AA:
 Query Match 89.0%; Score 1355; DB 24; Length 250;
 Best Local Similarity 100.0%; Pred. No. 7.6e-119;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 MRLQLILALATLNGGERRIINGFECKPSPQWQALPEKTLGATLIARMLLTA 92
 DB 1 MRLQLILALATLNGGERRIINGFECKPSPQWQALPEKTLGATLIARMLLTA 60
 QY 93 AHCLKPRIVYHLGQHNLOKEGCEQRTATSEFPHGFNNSLPKDHRNDIMLVKMASPV 152
 DB 61 AHCLKPRIVYHLGQHNLOKEGCEQRTATSEFPHGFNNSLPKDHRNDIMLVKMASPV 120
 QY 153 SITWAVRPLTLSSRCVYAGTSLISGWGSTSSPOLRLPHTLRCANITIIHOKCENAYPG 212
 DB 121 SITWAVRPLTLSSRCVYAGTSLISGWGSTSSPOLRLPHTLRCANITIIHOKCENAYPG 180
 QY 213 NITPTWVCASVOEGKSCSCGDSGGLVNCOSLOGIISWQDPCAIRKRGVYTKCKYV 272
 DB 181 NITPTWVCASVOEGKSCSCGDSGGLVNCOSLOGIISWQDPCAIRKRGVYTKCKYV 240
 QY 273 DWIOETMKN 282
 DB 241 DWIOETMKN 250
 RESULT 15
 ABU67098
 ID ABU67098 standard; Protein; 250 AA.
 XX
 AC ABU67098;
 XX
 DT 27-MAY-2003 (first entry)
 XX
 DE Human secreted/transmembrane, PRO, protein SEQ ID 506.
 XX

KW Human; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioreactor; tumour.
XX
OS Homo sapiens.
PN US2003032155-A1.
XX
PD 13-FEB-2003.
XX
PF 03-MAY-2002; 2002US-0137865.
XX
XX 31-MAR-1997; 97WO-US05330.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20944.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 22-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 05-JAN-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 10-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06319.
PR 20-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US07532.
PR 17-MAY-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15644.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0864280.
PR 25-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 01-JUN-2001; 2001US-0866034.
PR 05-JUN-2001; 2001US-0872035.
PR 14-JUN-2001; 2001US-0874503.
PR 19-JUN-2001; 2001US-0882636.
PR 21-JUN-2001; 2001US-0886342.
PR 18-JUL-2001; 2001US-0887879.
PR 06-AUG-2001; 2001US-0908827.
PR 09-AUG-2001; 2001US-0924419.
PR 16-AUG-2001; 2001US-0927796.
PR 19-DEC-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.

XX (GENTH) GENENTECH INC.
XX
PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-331925/31.
XX N-PSDB; ACN04276.
XX
DR New secreted and transmembrane nucleic acids and polypeptides,
XX designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer
XX
XX Claim 12; Fig 506; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid
CC further comprises the full-length coding sequence of the DNA deposited
CC under American Type Culture Collection (ATCC) accession number in a list
CC given in the specification. Also included are vectors and host
CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
CC antibodies, PRO extracellular domains and mature sequences, methods
CC of detecting PRO proteins, methods for stimulating the release of
CC TNF-alpha (tumour necrosis factor alpha) from human blood,
CC (and the proliferation of differentiation of chondrocyte cells, the
CC proliferation of, or gene expression in pericyte cells, the release or
CC proteoglycans from cartilage, proliferation of inner ear utricular
CC supporting cells, the proliferation of T-lymphocyte cells, the release
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the

CC proliferation of endothelial cells, a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumor in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.

XX Sequence 250 AA;

Query Match 89.0%; Score 1355; DB 24; Length 250;
 Best Local Similarity 100.0%; Pred. No. 7.6e-119;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	33	MRILQILILALATGLVGETRIIKGFCKPHSQPWQALFEKTRLLCGATLLAPRWLTA	92
DB	1	MRILQILILALATGLVGETRIIKGFCKPHSQPWQALFEKTRLLCGATLLAPRWLTA	60
QY	93	AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPV	152
DB	61	AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPV	120
QY	153	SITMAVRPLTLSPRCTAGTSCGISGSGTSSPOLRLPHTLRCANITTEHOKCENAYPG	212
DB	121	SITMAVRPLTLSPRCTAGTSCGISGSGTSSPOLRLPHTLRCANITTEHOKCENAYPG	180
QY	213	NITDTMVCASVOEGGKDCSQGDSGGPLVNCNLSGIIISWGDPCAITRKPGVYTVCKXV	272
DB	181	NITDTMVCASVOEGGKDCSQGDSGGPLVNCNLSGIIISWGDPCAITRKPGVYTVCKXV	240
QY	273	DWIOETMKKN	282
DB	241	DWIOETMKKN	250

Search completed: October 22, 2003, 15:51:33
 Job time : 43.9413 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2003, 15:50:17 ; Search time 27.0411 Seconds
(without alignments)
1746.375 Million cell updates/sec

Title: US-09-856-320a-2

Perfect score: 1523

Sequence: 1 MGRRLRLRDKSSGRLTAA.....GYTVKCKYVDWIGETMKNN 282

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1355	89.0	250	11	US-09-946-374-170 Sequence 170, App
2	1355	89.0	250	12	US-10-015-387A-170 Sequence 170, App
3	1355	89.0	250	12	US-10-137-870-506 Sequence 506, App
4	1355	89.0	250	12	US-10-140-018-506 Sequence 506, App
5	1355	89.0	250	12	US-10-140-021-506 Sequence 506, App
6	1355	89.0	250	12	US-10-140-274-506 Sequence 506, App
7	1355	89.0	250	12	US-10-140-471-506 Sequence 506, App
8	1355	89.0	250	12	US-10-140-807-506 Sequence 506, App
9	1355	89.0	250	12	US-10-140-922-506 Sequence 506, App
10	1355	89.0	250	12	US-10-140-924-506 Sequence 506, App
11	1355	89.0	250	12	US-10-140-926-506 Sequence 506, App
12	1355	89.0	250	12	US-10-141-698-506 Sequence 506, App
13	1355	89.0	250	12	US-10-141-702-506 Sequence 506, App
14	1355	89.0	250	12	US-10-141-704-506 Sequence 506, App
15	1355	89.0	250	12	US-10-142-421-506 Sequence 506, App

16	1355	89.0	250	12	US-10-142-432-506 Sequence 506, App
17	1355	89.0	250	12	US-10-142-767-506 Sequence 506, App
18	1355	89.0	250	12	US-10-143-033-506 Sequence 506, App
19	1355	89.0	250	12	US-10-144-994-506 Sequence 506, App
20	1355	89.0	250	12	US-10-145-628-506 Sequence 506, App
21	1355	89.0	250	12	US-10-145-631-506 Sequence 506, App
22	1355	89.0	250	12	US-10-145-633-506 Sequence 506, App
23	1355	89.0	250	12	US-10-145-746-506 Sequence 506, App
24	1355	89.0	250	12	US-10-145-748-506 Sequence 506, App
25	1355	89.0	250	12	US-10-145-823-506 Sequence 506, App
26	1355	89.0	250	12	US-10-145-826-506 Sequence 506, App
27	1355	89.0	250	12	US-10-145-870-506 Sequence 506, App
28	1355	89.0	250	12	US-10-145-876-506 Sequence 506, App
29	1355	89.0	250	12	US-10-145-959-506 Sequence 506, App
30	1355	89.0	250	12	US-10-146-724-506 Sequence 506, App
31	1355	89.0	250	12	US-10-146-725-506 Sequence 506, App
32	1355	89.0	250	12	US-10-146-795-506 Sequence 506, App
33	1355	89.0	250	12	US-10-146-795-506 Sequence 506, App
34	1355	89.0	250	12	US-10-147-495-506 Sequence 506, App
35	1355	89.0	250	12	US-10-147-501-506 Sequence 506, App
36	1355	89.0	250	12	US-10-147-504-506 Sequence 506, App
37	1355	89.0	250	12	US-10-147-506-506 Sequence 506, App
38	1355	89.0	250	12	US-10-147-509-506 Sequence 506, App
39	1355	89.0	250	12	US-10-147-510-506 Sequence 506, App
40	1355	89.0	250	12	US-10-147-511-506 Sequence 506, App
41	1355	89.0	250	12	US-10-147-529-506 Sequence 506, App
42	1355	89.0	250	12	US-10-152-397-506 Sequence 506, App
43	1355	89.0	250	12	US-10-153-586-506 Sequence 506, App
44	1355	89.0	250	12	US-10-158-783-506 Sequence 506, App
45	1355	89.0	250	12	US-10-158-786-506 Sequence 506, App
					US-10-006-130A-170 Sequence 170, App

ALIGNMENTS

RESULT 1
US-09-946-374-170
Sequence 170, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Bortstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946.374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750


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; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

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Query Match      89.0%; Score 1355; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126; Indels 0; Gaps 0;
Matches 250; Conservative 0; Mismatches 0;

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QY 33 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWQALFEKTRLLCGATLLAPRWLLTA 92
DB 1 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWQALFEKTRLLCGATLLAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 120
QY 153 SITMAVRPLTSSRCVTAGTSCISGWSSTSSPOLRPLPTLRCANTITIEHOKCENAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCISGWSSTSSPOLRPLPTLRCANTITIEHOKCENAYPG 180
QY 213 NITDVMCASVOEGKDSQGDGSGPLVNCOSLOGIISWGODPCATRRKPGVYTKVKYV 272
DB 181 NITDVMCASVOEGKDSQGDGSGPLVNCOSLOGIISWGODPCATRRKPGVYTKVKYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

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RESULT 2

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US-10-015-387A-170
; Sequence 170, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; PRIOR FILING DATE: 2001-12-12
; PRIOR Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 170
; LENGTH: 250
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-015-387A-170

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Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126; Indels 0; Gaps 0;
Matches 250; Conservative 0; Mismatches 0;

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QY 33 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWQALFEKTRLLCGATLLAPRWLLTA 92
DB 1 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWQALFEKTRLLCGATLLAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 120
QY 153 SITMAVRPLTSSRCVTAGTSCISGWSSTSSPOLRPLPTLRCANTITIEHOKCENAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCISGWSSTSSPOLRPLPTLRCANTITIEHOKCENAYPG 180
QY 213 NITDVMCASVOEGKDSQGDGSGPLVNCOSLOGIISWGODPCATRRKPGVYTKVKYV 272
DB 181 NITDVMCASVOEGKDSQGDGSGPLVNCOSLOGIISWGODPCATRRKPGVYTKVKYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

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RESULT 3

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US-10-137-870-506
; Sequence 506, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:

```

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C155
; CURRENT APPLICATION NUMBER: US/10/137,870
; PRIOR FILING DATE: 2002-05-03
; PRIOR Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-506

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Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126; Indels 0; Gaps 0;
Matches 250; Conservative 0; Mismatches 0;

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QY 33 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWQALFEKTRLLCGATLLAPRWLLTA 92
DB 1 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWQALFEKTRLLCGATLLAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 152

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Db      61 AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKMASPV 120
QY      153 SITWAVRPLTSSRCVTAAGTSCGISGSGTSSPOLRLPHTLRCAITITIEHOKCENAYPG 212
Db      121 SITWAVRPLTSSRCVTAAGTSCGISGSGTSSPOLRLPHTLRCAITITIEHOKCENAYPG 180
QY      213 NITDTMVCASVOEGGKSCQDGSGLVNCNOSLGGIISWGDDPCAITRKPGVYTKVCKYV 272
Db      181 NITDTMVCASVOEGGKSCQDGSGLVNCNOSLGGIISWGDDPCAITRKPGVYTKVCKYV 240
QY      273 DWIOETMKNN 282
Db      241 DWIOETMKNN 250

RESULT 4
US-10-140-018-506
; Sequence 506, Application US/10140018
; Publication No. US20030138865A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-018-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,36-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 MRLIQLILALATGIVGGETRIIKGFECCKPSQPMQALFEXTRLGCAITLIAPRWLTA 92
Db      1 MRLIQLILALATGIVGGETRIIKGFECCKPSQPMQALFEXTRLGCAITLIAPRWLTA 60
QY      93 AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKMASPV 152
Db      61 AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKMASPV 120
QY      153 SITWAVRPLTSSRCVTAAGTSCGISGSGTSSPOLRLPHTLRCAITITIEHOKCENAYPG 212
Db      121 SITWAVRPLTSSRCVTAAGTSCGISGSGTSSPOLRLPHTLRCAITITIEHOKCENAYPG 180
QY      213 NITDTMVCASVOEGGKSCQDGSGLVNCNOSLGGIISWGDDPCAITRKPGVYTKVCKYV 272
Db      181 NITDTMVCASVOEGGKSCQDGSGLVNCNOSLGGIISWGDDPCAITRKPGVYTKVCKYV 240
QY      273 DWIOETMKNN 282
Db      241 DWIOETMKNN 250
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```
RESULT 5
US-10-140-021-506
; Sequence 506, Application US/10140021
; Publication No. US20030138866A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-021-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,36-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 MRLIQLILALATGIVGGETRIIKGFECCKPSQPMQALFEXTRLGCAITLIAPRWLTA 92
Db      1 MRLIQLILALATGIVGGETRIIKGFECCKPSQPMQALFEXTRLGCAITLIAPRWLTA 60
QY      93 AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKMASPV 152
Db      61 AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKMASPV 120
QY      153 SITWAVRPLTSSRCVTAAGTSCGISGSGTSSPOLRLPHTLRCAITITIEHOKCENAYPG 212
Db      121 SITWAVRPLTSSRCVTAAGTSCGISGSGTSSPOLRLPHTLRCAITITIEHOKCENAYPG 180
QY      213 NITDTMVCASVOEGGKSCQDGSGLVNCNOSLGGIISWGDDPCAITRKPGVYTKVCKYV 272
Db      181 NITDTMVCASVOEGGKSCQDGSGLVNCNOSLGGIISWGDDPCAITRKPGVYTKVCKYV 240
QY      273 DWIOETMKNN 282
Db      241 DWIOETMKNN 250

RESULT 6
US-10-140-274-506
; Sequence 506, Application US/10140274
; Publication No. US20030143674A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
```

```

; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-274-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MIIQLIILALATGLVGSTRITIKGFECKPHSQPMQALFEKTRLLCGATLIAPRWLTA 92
Db 1 MIIQLIILALATGLVGSTRITIKGFECKPHSQPMQALFEKTRLLCGATLIAPRWLTA 60

QY 93 AHCLKPRYIVHLGOHNLQKEGCEOTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 152
Db 61 AHCLKPRYIVHLGOHNLQKEGCEOTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 120

QY 153 SITMAVRPLTSSRCVTAGTSCSLISGWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPG 212
Db 121 SITMAVRPLTSSRCVTAGTSCSLISGWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPG 180

QY 213 NITDTMVCASVOEGKDCSQGDSGGLVLCNOSLQGIISWGDPICATITRRPGVYTVCKXV 272
Db 181 NITDTMVCASVOEGKDCSQGDSGGLVLCNOSLQGIISWGDPICATITRRPGVYTVCKXV 240

QY 273 DWIOETMKNN 282
Db 241 DWIOETMKNN 250

RESULT 7
US-10-140-471-506
; Sequence 506, Application US/10140471
; Publication No. US20030138887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
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; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-471-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MIIQLIILALATGLVGSTRITIKGFECKPHSQPMQALFEKTRLLCGATLIAPRWLTA 92
Db 1 MIIQLIILALATGLVGSTRITIKGFECKPHSQPMQALFEKTRLLCGATLIAPRWLTA 60

QY 93 AHCLKPRYIVHLGOHNLQKEGCEOTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 152
Db 61 AHCLKPRYIVHLGOHNLQKEGCEOTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 120

QY 153 SITMAVRPLTSSRCVTAGTSCSLISGWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPG 212
Db 121 SITMAVRPLTSSRCVTAGTSCSLISGWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPG 180

QY 213 NITDTMVCASVOEGKDCSQGDSGGLVLCNOSLQGIISWGDPICATITRRPGVYTVCKXV 272
Db 181 NITDTMVCASVOEGKDCSQGDSGGLVLCNOSLQGIISWGDPICATITRRPGVYTVCKXV 240

QY 273 DWIOETMKNN 282
Db 241 DWIOETMKNN 250
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RESULT 8
US-10-140-807-506
; Sequence 506, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-807-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
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Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLIQLILALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
Db 1 MRLIQLILALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60

QY 93 AHCLKPRYIVHIGQHNLOKEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
Db 61 AHCLKPRYIVHIGQHNLOKEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120

QY 153 SITWAVRPLTSSRCVTAAGTSCGISGWSSTSSPOLRPHLTRCANITIIIEHOKCENAYPG 212
Db 121 SITWAVRPLTSSRCVTAAGTSCGISGWSSTSSPOLRPHLTRCANITIIIEHOKCENAYPG 180

QY 213 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKXY 272
Db 181 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKXY 240

QY 273 DWIOETMKN 282
Db 241 DWIOETMKN 250

RESULT 9

US-10-140-922-506
; Sequence 506, Application US/10140922
; Publication No. US20030138889A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C179
; CURRENT APPLICATION NUMBER: US/10/140,922
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-922-506

Query Match 89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLIQLILALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
Db 1 MRLIQLILALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60

QY 93 AHCLKPRYIVHIGQHNLOKEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
Db 61 AHCLKPRYIVHIGQHNLOKEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120

QY 153 SITWAVRPLTSSRCVTAAGTSCGISGWSSTSSPOLRPHLTRCANITIIIEHOKCENAYPG 212
Db 121 SITWAVRPLTSSRCVTAAGTSCGISGWSSTSSPOLRPHLTRCANITIIIEHOKCENAYPG 180

QY 213 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKXY 272
Db 181 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKXY 240

QY 273 DWIOETMKN 282
Db 241 DWIOETMKN 250

RESULT 10

US-10-140-924-506
; Sequence 506, Application US/10140924
; Publication No. US20030134355A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C177
; CURRENT APPLICATION NUMBER: US/10/140,924
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-924-506

Query Match 89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLIQLILALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
Db 1 MRLIQLILALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60

QY 93 AHCLKPRYIVHIGQHNLOKEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
Db 61 AHCLKPRYIVHIGQHNLOKEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120

QY 213 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKXY 272
Db 181 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKXY 240

QY 273 DWIOETMKN 282
Db 241 DWIOETMKN 250

RESULT 11

US-10-140-926-506
; Sequence 506, Application US/10140926

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Publication No. US20030134356A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C187
CURRENT APPLICATION NUMBER: US/10/140,926
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-926-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 33 MRILQLILALATGLVGETRIIKGFECCKPHSQPQAALEFEXTRLLCGATLLIAPRWLLTA 92
DB 1 MRILQLILALATGLVGETRIIKGFECCKPHSQPQAALEFEXTRLLCGATLLIAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEGCEQRTATSFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEGCEQRTATSFPHPGFNNSLPNKDHRNDIMLVKMASPV 120
QY 153 SITWAVRPLTSSRCVTAGTSCLSISGWGSTSSPOLRLPHTLRCAITIIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCLSISGWGSTSSPOLRLPHTLRCAITIIIEHOKCENAYPG 180
QY 213 NITDTMVCASVOEGGKDCSQDGGSGPLVCNOSLQGIISWGDDPCAITRKPGVYTVCKYV 272
DB 181 NITDTMVCASVOEGGKDCSQDGGSGPLVCNOSLQGIISWGDDPCAITRKPGVYTVCKYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

RESULT 12
US-10-141-698-506
Sequence 506, Application US/10141698
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
```

```
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C206
CURRENT APPLICATION NUMBER: US/10/141,698
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-698-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 33 MRILQLILALATGLVGETRIIKGFECCKPHSQPQAALEFEXTRLLCGATLLIAPRWLLTA 92
DB 1 MRILQLILALATGLVGETRIIKGFECCKPHSQPQAALEFEXTRLLCGATLLIAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEGCEQRTATSFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEGCEQRTATSFPHPGFNNSLPNKDHRNDIMLVKMASPV 120
QY 153 SITWAVRPLTSSRCVTAGTSCLSISGWGSTSSPOLRLPHTLRCAITIIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCLSISGWGSTSSPOLRLPHTLRCAITIIIEHOKCENAYPG 180
QY 213 NITDTMVCASVOEGGKDCSQDGGSGPLVCNOSLQGIISWGDDPCAITRKPGVYTVCKYV 272
DB 181 NITDTMVCASVOEGGKDCSQDGGSGPLVCNOSLQGIISWGDDPCAITRKPGVYTVCKYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

RESULT 13
US-10-141-702-506
Sequence 506, Application US/10141702
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C208
CURRENT APPLICATION NUMBER: US/10/141,702
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
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; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-702-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 MRIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
DB 1 MRIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60
OY 93 AHCLKPRYIVHLGQHNLOKEGCEQOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEGCEQOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120
OY 153 SITMAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 180
OY 213 NITDTMVCASVOEGGKDCSQDSCGPLYVNCNSLOGIISWGODPCAITRKPGVYTKVCXYV 272
DB 181 NITDTMVCASVOEGGKDCSQDSCGPLYVNCNSLOGIISWGODPCAITRKPGVYTKVCXYV 240
OY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

RESULT 14
US-10-141-704-506
; Sequence 506, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C209
; CURRENT APPLICATION NUMBER: US/10/141,704
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-704-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 MRIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
DB 1 MRIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60
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OY 93 AHCLKPRYIVHLGQHNLOKEGCEQOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEGCEQOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120
OY 153 SITMAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 180
OY 213 NITDTMVCASVOEGGKDCSQDSCGPLYVNCNSLOGIISWGODPCAITRKPGVYTKVCXYV 272
DB 181 NITDTMVCASVOEGGKDCSQDSCGPLYVNCNSLOGIISWGODPCAITRKPGVYTKVCXYV 240
OY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

RESULT 15
US-10-142-421-506
; Sequence 506, Application US/10142421
; Publication No. US20030134360A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C218
; CURRENT APPLICATION NUMBER: US/10/142,421
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-421-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 MRIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
DB 1 MRIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60
OY 93 AHCLKPRYIVHLGQHNLOKEGCEQOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEGCEQOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120
OY 153 SITMAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 180
OY 213 NITDTMVCASVOEGGKDCSQDSCGPLYVNCNSLOGIISWGODPCAITRKPGVYTKVCXYV 272
DB 181 NITDTMVCASVOEGGKDCSQDSCGPLYVNCNSLOGIISWGODPCAITRKPGVYTKVCXYV 240
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Oy	273	DWIOETMKN	282
Db	241	DWIOETMKN	250

Search completed: October 22, 2003, 15:54:43
Job time : 30.0411 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 23, 2003, 14:05:42 ; Search time 310.145 Seconds
(without alignments)
2454.471 Million cell updates/sec

Title: US-09-856-320A-2
Perfect score: 1523
Sequence: 1 MGRRLWRMDKSSGRGLTAA.....GYTVKVCYVDVIGETMKNN 282

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 2552756 segs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=N.Geneseq.19Jun03 -QFMT=fasted -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
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-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09856320.@cgn_1.1.401@runac.22102003.121413.25652 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1523	100.0	1106	20	AA222638	CASB12 nucleotide
2	1523	100.0	1158	20	AA222639	CASB12 derived fro
3	1523	100.0	1186	24	ABK92131	Prostate cancer-as
4	1523	100.0	1186	25	ABK76468	Lung cancer-associ
5	1523	100.0	1204	21	AAA317072	Human PRO1279 (UNQ
6	1523	100.0	1204	22	AA521496	Human cDNA sequenc
7	1523	100.0	1204	22	AAPE54320	DNA encoding prote
8	1523	100.0	1204	24	ABL95664	Human angiogenesis
9	1523	100.0	1204	24	ABL88175	Human PRO1279 cDNA
10	1523	100.0	1204	24	ABK33628	CDSNA encoding huma
11	1523	100.0	1204	25	ACA03855	CDSNA encoding huma
12	1523	100.0	1204	25	ACA04276	Human cDNA encodin
13	1523	100.0	1204	25	ABX89393	DNA encoding novel
14	1523	100.0	1301	21	AAA61763	CDSNA encoding huma
15	1523	100.0	1314	21	AA230222	CDSNA encoding a hu
16	1519	99.7	1292	22	ABA83372	Human secreted pro
17	1492.5	98.0	1135	21	AA245672	Nucleotide sequenc
18	1410	92.6	1192	22	AA214842	Human PS133 consen
19	1398	91.8	1166	22	AA214841	CDSNA encoding huma
20	1388.5	91.2	934	21	AAA61765	Extended human sec
21	1380	90.6	1191	20	AAK97777	Human secreted pro
22	1284	84.3	1146	20	AAV84589	Human secreted pro
23	1284	84.3	1146	22	ABA83430	Human secreted pro
24	1279.5	84.0	1164	24	AB551683	DNA encoding human
25	1233	81.0	833	19	AAV42925	DNA encoding a hum
26	1237	80.6	1052	21	AAK87798	Activation consen
27	1227	80.6	1052	22	AAK55270	Nucleotide sequenc
28	1187	77.9	1323	21	AAK61764	CDSNA encoding mous
29	981	64.4	762	21	AAH31050	Human colon cancer
30	981	64.4	762	21	AAH31061	Human colon cancer
31	916.5	60.2	618	24	ABK30233	Human G-protein-co
32	769.5	50.5	1438	24	ABO99855	Human coding seque
33	758	49.8	1375	22	ABK26876	Human cDNA encodin
34	754	49.5	1365	22	AA541087	CDSNA encoding nove
35	739	48.5	472	24	ABK30366	Human G-protein-co
36	736	48.3	924	22	AA541622	CDSNA encoding nove
37	736	48.3	924	22	AA526948	Human cDNA encodin
38	736	48.3	924	23	ABK41855	CDSNA encoding nove
39	698.5	45.9	1322	17	AB199534	Mouse ischaemic co
40	698.5	45.9	1333	14	AAT48519	Human neuropsin-en
41	698.5	45.9	1333	18	AAT63251	Mouse neuropsin ge
42	696	45.7	963	24	AA230570	Human protease, PR
43	696	45.7	963	24	ABK31774	DNA encoding novel
44	692.5	45.5	1278	24	ABK46347	CDSNA encoding nove
45	690.5	45.3	1343	20	AAK28633	Nucleotide sequenc

ALIGNMENTS

RESULT 1
AA222638
ID AA222638 standard; cDNA, 1106 BP.
AC AA222638;
XX
DT 08-DEC-1999 (first entry)
XX
DE CASB12 nucleotide sequence.
XX
XX neuropsin; cancer; assay; inhibitor; serine protease; immunogenic;
KW ds.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 14..862

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FT      /tag= a
FT      /product= CASB12
XX      WO9949055-A1.
XX      30-SEP-1999.
XX      PD
XX      17-MAR-1999; 99WO-EP01894.
XX      PR
XX      20-MAR-1998; 98GB-0006095.
XX      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX      PA
XX      PI Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;
XX      DR WPI; 1999-580450/49.
XX      DR P-PSDB; AAY42439.
XX      PT New human serine protease CASB12, for treatment, prevention and
XX      diagnosis of cancer and autoimmune diseases.
XX      PS Claim 10; Page 47; 58pp; English.
XX      CC This is the nucleotide sequence of the CASB12 gene. The nucleotide
XX      CC sequence of AA222638 shows homology with neuropilin and the encoded
XX      CC protein AA142439 is structurally related to other proteins of the
XX      CC serine protease family, having homology and/or structural similarity
XX      CC with neuropilin. It is expected that as well as similar structure, these
XX      CC proteins will also share similar biological functions and properties.
XX      CC The CASB12 polypeptides and polynucleotides can be used to develop
XX      CC methods for identifying agonists and antagonists/inhibitors of these
XX      CC molecules, and thereby treating conditions associated with CASB12
XX      CC polypeptide imbalance. The invention also provides for diagnostic assays
XX      CC for detecting diseases associated with inappropriate CASB12 polypeptide
XX      CC activity or levels.
XX      CC Since CASB12 is either specifically expressed or highly over-expressed
XX      CC in tumors compared to normal cells, the polypeptides and polynucleotides
XX      CC of the invention are believed to be important immunogens for specific
XX      CC prophylactic or therapeutic immunization against tumors. The
XX      CC polypeptides and polynucleotides can therefore be targeted by antigen
XX      CC specific immune reactions (which result in the destruction of the tumor
XX      CC cell) or they can be used to diagnose the occurrence of tumor cells.
XX      SQ Sequence 1106 BP, 247 A; 348 C; 287 G; 224 T; 0 other;

Alignment Scores:
Pred. No.: 2,24e-122 Length: 1106
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-856-320A-2 (1-282) x AA222638 (1-1106)
QY      1 MetGlnAArgLeuAArgTrpLeuAArgAspTrpLysSerSerGlyAArgGlyLeuThrAla 20
DB      14 ATGCAGAGGCTTACGAGTGGCTGCGGAGCTGGAAGTATCATCGGCGAGAGTCTCACAGAGC 73
QY      21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
DB      74 AAGGAACCTGGGGCCGCTCTCCCTCCCGAGGCAATGAGGATTTCTGAGTTAAATCTTG 133
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLysGlyPheGluCys 60
DB      134 CTTCCTCTGGCAACAGGGCTTGTAGGGGAGAGACAGATATCATCAGGGGTTCCAGTGC 193
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuCysGly 80
DB      194 AAGCTCTACCTCCACCCCTGCGAGGAGCCCTGTTGAGAAACACCGGCTACTCTGTGGG 253
QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100

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DB      254 GCGAGCTCATCGCCCCAGATGGCTCTGTACACAGCCCACTGCTCAAGCCCCGCTAC 313
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnThrArgThr 120
DB      314 ATAGTTACACTGGGGGACACACACTCCAGAAAGAGAGGGGCTGTGAGACACCCGAGACA 373
QY      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB      374 GCCACTGAGTCTTCTCCCGACCCGCGCTTCAACAACACCTTCCCAACAAAGACCCACCGC 433
QY      141 AsnAspIleMetLeuValIleValMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB      434 AATGACATCATGCTCTGTGTAAGATGGATGCCAGCTTCATCACCCTGGCTGTGAGACC 493
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
DB      494 CTCACCTCTCTCTCAGCTGTGTGTCACGCTGTGACACAGCTGCTCATTTCCGGCTGGGGC 553
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB      554 AGCAGTCTCACGCCCCAGATTACGCTGCTTACACCTTGCGATGCGCCAAACATCACCATC 613
QY      201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrArgSerThrMetValCys 220
DB      614 ATTGAGCACCGAAGTGTGAGAACGCTTACCCCGGCAACATCACAGACACCATGTGTGT 673
QY      221 AlaSerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
DB      674 GCCAGCGTGCAGGAAGGGGGCAAGAGACTCTGCCACAGGTGACTCCGGGGCCCTGTGTC 733
QY      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB      734 TGTAAACGATGCTCTTCAAGGATTAATCTCTGGGGCCAGAGTCCGTGCGATATCACCGGA 793
QY      261 LysProGlyValTyrThrLysValCysLeuValAspTrpIleGlnGluThrMetLys 280
DB      794 AAGCTGTGTCTACAGAAAGTCTGCAAAATATGTGAGCTGATCCAGAGACCATGTAG 853
QY      281 AsnAsn 282
DB      854 AACCAAT 859

RESULT 2
AA222639
ID      AA222639 standard; cDNA; 1158 BP.
XX      AC
XX      AA222639;
XX      DT 08-DEC-1999 (first entry)
XX      DE CASB12 derived from Expressed Sequence Tag sequences.
XX      KW neuropilin; cancer; assay; inhibitor; serine protease; immunogenic;
XX      KW autoimmune disease; ds.
XX      OS Homo sapiens.
XX      FH
XX      Key Location/Qualifiers
XX      CDS 84..932
XX      FT /tag= a
XX      FT /product= CASB12
XX      PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX      PI Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;

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XX Claim 22; Page 313; 436pp; English.
 CC The present invention relates to methods of detecting a prostate
 CC cancer-associated transcript in a cell from a patient. The method
 CC comprises contacting a biological sample from the patient with
 CC prostate cancer-associated polynucleotides (designated PC genes) that
 CC selectively hybridize to a sequence that is at least 80% identical
 CC to them. The prostate cancer-associated polynucleotide sequences
 CC are differentially expressed in prostate tumour tissue or in
 CC prostate cancer and are derived from the tissues of various
 CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
 CC The methods of the invention are useful for diagnosing and treating
 CC prostate cancer in mammals. The prostate cancer-associated genes are
 CC useful for diagnosing or treating prostate cancer, as well as for
 CC identifying modulators of prostate cancer or agents that inhibit
 CC prostate cancer. The nucleic acid sequences are particularly useful
 CC in gene therapy, as a vaccine or in antisense applications.
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
 CC sequences.

XX SQ Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other;

Alignment Scores:

Pred. No.: 2,45e-122 Length: 1186
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-856-320A-2 (1-282) x ABK92131 (1-1186)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
 DB 26 ATGCGAGGTTAGAGTGGCTGGCGGAGCTGGAAGTATATCGGCGAGCTTCACAGCAGC 85
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
 DB 86 AAGGAACCTGGGGCGGCTCTCCCTCCAGCCATAGAGATTCTGCAGTTAATCTCG 145
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
 DB 146 CTGGCTCTGGCAACAGGCTTGAAGGGAGAGAGACCAAGATATCAAGGGGTTCAAGTCC 205
 QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLeuThrArgLeuLeuGlyGly 80
 DB 206 AAGCTCACTCCAGGCTGGAGGAGAGGCTGTTGAGAAACAGCGGCTACTGTGTGG 265
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 266 GCGAGCGCTATGCGCCCGATGGCTCTCGACAGAGCCCACTGCTCAAGCCCGCTAC 325
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 DB 326 ATAGTTCACTGGGGAGCAACCTCCGAAGAGAGAGGCTGTGAGCAGACCGGACA 385
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 386 GGCACGTAGTCTTCCCAACCCCGGCTTCACACAGCTCCCAACACCAACACACCCG 445
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTyrAlaValArgPro 160
 DB 446 AATGACATCATGCTGGTGAAGATGGATGGCAGTCTCATCACTGGGCTGTGCAGACC 505
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrProGly 180
 DB 506 CTCACCTCTCTCCACGCTGTCTACTGTGACACCAAGTGTCTATTTCCGGCTGGGCG 565
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 DB 566 AGCAGCTCCAGCCCAAGTTAGCGCTGCTCACACCTTGCGATGGCCCAACATCACCATC 625

QY 201 IleGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
 DB 626 ATTGAGCCACCAAGTGTGAGAAAGCCCTTACCCCGCAACATCAACAGACCATGCTGTGT 685
 QY 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
 DB 686 GCCACGCTGCAGGAAGGGGGCAAGGACTCTCCAGGGGTGACTCCGGGGCCCTCTGGTTC 745
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
 DB 746 TGTAACCACTCTCTTCAAGGATTAATCTCTGGGGCCAGATCCGTGTGCATCACCCGA 805
 QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
 DB 806 AAGCTGTGTCTACACCAAGTGTGCMAAATGTGTGACTGATTCACAGACCATGTAAG 865
 QY 281 AsnAsn 282
 DB 866 AACCAAT 871

RESULT 4

ABX76468 standard; DNA; 1186 BP.

ABX76468;
 02-APR-2003 (first entry)

Lung cancer-associated polynucleotide #32.

Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
 antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;
 small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

Unidentified.

WO200286443-A2.

31-OCT-2002.

18-APR-2002; 2002WO-US12476.

18-APR-2001; 2001US-284770P.

10-MAY-2001; 2001US-290492P.

09-NOV-2001; 2001US-339245P.

13-NOV-2001; 2001US-350666P.

29-NOV-2001; 2001US-334370P.

12-APR-2002; 2002US-372246P.

(EOSB-) EOS BIOTECHNOLOGY INC.

Aziz N. Murray R;

WPI; 2003-093161/08.

P-PSDB; ABUS6739.

Detecting a lung cancer-associated transcript in a cell from a patient

for treating lung cancer, by contacting a biological sample from the

patient with a polynucleotide that exhibits increased or decreased

expression in lung cancer -

Claim 22; Page 443; 453pp; English.

The invention relates to a method for detecting a lung cancer-associated

transcript in a cell from a patient, comprising contacting a biological

sample from the patient with a polynucleotide that selectively hybridises

to a sequence that is at least 80 % identical to a gene that exhibits

increased or decreased expression in lung cancer samples. Lung

cancer-associated polynucleotides and polypeptides are used for

identifying a compound that modulates a lung cancer-associated

polypeptide, for inhibiting proliferation of a lung cancer-associated


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PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102310.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102687.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0106500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.

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PR 17-NOV-1998; 98US-0108867.
PR 17-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108948.
PR 18-NOV-1998; 98US-0108949.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.
XX (GETH ) GENENTECH INC.
XX
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX WPI, 2000-237871/20.
XX P-PSDB; AAY99390.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or
XX secreted PRO polypeptides, useful for screening of potential peptide or
XX small molecule inhibitors of the relevant receptor/ligand interactions
XX
XX Claim 2, Fig 101, 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding them have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37310 represent
XX PCR primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention.
XX
XX SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:
PR No.: 2,5e-122 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-856-320A-2 (1-282) x AAA37072 (1-1204)
QY 1 MetGlnArgLeuAaGTrpLeuAaGAspTrpLysSerSergIyArgGlyLeuThrAla 20
DB 10 ATGCAAGAGTTGAGGTGCTGCGGAGCTGAAGTCATCGGCGAGGCTTCACAGCACC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleuGlnLeu 40
DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCCCAAGAGATTCGACGTAACTCTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlnThrArgIleIleGlyPheGly 60
DB 130 CTGCTCGGCAACAGGCTTGTAGGGGAGAGACAGACATCAAGGCTTCAGTCC 189
QY 61 LysProHisSergInProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuGly 80
DB 190 AAGCTCACTCCAGCCCTGCGAGGACGCTGTTCGAGAGAGCGGCTCTCTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGCTCATCGCCCGCAGATGCTCTGACACAGCCCACTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyGlyGlnGlnThr 120
DB 310 ATAGTTCACTCGGGCGACCAACCTCCAGAGAGAGAGGCTGTGACCAACCCGCA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACTGAGTCTTCCCCCAACCCGCGCTTCAACAACAGCCTCCCAACAAGACCAACCGC 429

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QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db 430 AATGACATCATCTGCTGGAAGATGGCATCGCCAGCTCCATCATCTGGGTGGCAGCC 489
QY 161 LeuThrLeuSerSerArgCysValIleThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db 490 CTCACCTCTCCCTCAGCGTGTGTCTGCTGCGGACAGCTGCTCATTTCCGGCTGGGCG 549
QY 181 SerThrSerSerProGlnLeuValGluLeuProIleThrLeuArgCysAlaAsnIleThrIle 200
Db 550 AGACCTCCAGCCCCCAGTTACCGCTGCTCCACACCTTGCGAGTCCGCCAATCACCACATC 609
QY 201 IleGlnHisGlnLysCysGluAsnAlaIleTyrProGlyAsnIleThrAspThrMetValCys 220
Db 610 ATTGACACACAGAAAGTGTGAACGCTACCCCGGCAACATCAGACACCAATGGTGTG 669
QY 221 AlaSerValGlnGluGlyValLysAspSerCysGlnGlyAspSerGlyValProLeuVal 240
Db 670 GCCAGGCTCAGAGAGAGGGGCAAGGACTCTGCGAGGTCATCCCGGGGCGCTCTGCTC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db 730 TGTAACTAGTCTCTTAAGGCAATTATCTCTGSGGCGAGGATCCGTGCGATCACCCGA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnIleThrMetLys 280
Db 790 AAGCCTGGTGTCTACAGCAAGCTCTCAATATATGTGACTGGATCCAGAGAGATGAAG 849
QY 281 AsnAsn 282
Db 850 AACCAAT 855

RESULT 6
AAS21496
ID AAS21496 standard; cDNA; 1204 BP.
AC AAS21496;
XX
XX 24-OCT-2001 (first entry)
DT
XX
XX Human cDNA sequence encoding for PRO1279 polypeptide.
DE
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX MO200140466-A2.
PN
XX
XX 07-JUN-2001.
PD
XX
XX 01-DEC-2000; 2000WO-US32678.
PF
XX
XX 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.

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PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
XX (GENTH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
PI Gertsen ME, Goddard A, Godowski RJ, Gunney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-408281/43.
DR P-PSDB; AAU12424.
XX
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
XX Claim 3; Fig 505; 813pp; English.
XX
XX AAS21244-AAS21518 encode for novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood; the
CC gene expression or differentiation of chondrocytes; the proliferation or
CC gene expression in pericyte cells; the release of proteoglycans from
CC cartilage; the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes; the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
XX SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:
Pred. No.: 2,56-122 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-856-320A-2 (1-282) x AAS21496 (1-1204)
QY 1 MetGlnArgLeuArgTrpLeuValArgAspTrpLysSerSerGlyValArgIleuThrAla 20
Db 10 ATGCAGAGCTTACGCTGCTGCGGAGCTGGAAGTATATGGGAGAGGCTCTCAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuLeu 40
Db 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCAATGAGATTCGAGTTAATCTCTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlyThrArgGlyIleLeuGlyPheGlyCys 60
Db 130 CTGCTCTGGGACAGGCTGTGTAGGGGAGAGCAGAGATATCAAGGGGTTCAAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaIleuPheGlyLysThrArgLeuLeuCysGly 80

```

```

Db      190 AAGCTCACTCCAGCCCTGGAGGAGCCCTGTTGAGAGAACGGGCTACTGTGGG 249
QY      81 AATATTTTLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250 GGGAGCGCTCATGCCCCCAGATGGCTCCGACAGCAGCCACTGCTCAAGCCCCGCTAC 309
QY      101 ILeValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysGlnGlnThrArgThr 120
Db      310 ATAGTTTCACTGGGGGAGCACAACCTCCAGAGAGAGAGAGGCTGTGAGCAGACCCGAGCA 369
QY      121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCCACTGAGTCTTCCCCCAGCCCGGCTTCAACAACAGCTCCCAACAAGAACACCGCC 429
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db      430 AATGACATCATCTGCTGTAAGATGGCATGCCAGTCTCCATCACCCTGGGCTGTGACCC 489
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db      490 CTCACCTCTCTCTCAAGCTGTGTCTACTGCTGGACACCACTGCTCATTTCCGGCTGGGC 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550 AGCAGCTCCAGCCCAAGTTAGCCTGCTCAGCTTGCATGCCGCAACATCACCATC 609
QY      201 ILeGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
Db      610 ATTGAGACACCAAGATGTAGAAAGCGCTACCCCGGCAACATCACAGACCATGTGTGT 669
QY      221 AlaSerValGlnGlnGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
Db      670 GCCACGCTGCAGAGAGGGGCAAGACTCTCTCCAGGGGACTCCGGGGCCCTTGGTC 729
QY      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db      730 TGTAACTGCTCTTCAAGGCATTTATCTCTCTGGGGCAGAGATCCGTTGCCATCACCCGA 789
QY      261 LysProGlyValIleThrLysValCysLysIleValAspTrpIleGlnGlnThrMetLys 280
Db      790 AAGCTGTGTCTACACGAAAGTGTGCAAAATATGTGACTGATCAGAGACGATGTAAG 849
QY      281 AsnAsn 282
Db      850 AACCAAT 855

RESULT 7
AAF54320
ID      AAF54320 standard; DNA; 1204 BP.
XX      AC      AAF54320;
XX      DT      02-APR-2001 (first entry)
XX      DE      DNA encoding protein of the invention #51.
XX      KW      Secreted; transmembrane; gene therapy; ss.
XX      OS      Unidentified.
XX      PN      WO200078961-A1.
XX      PD      28-DEC-2000.
XX      PF      18-FEB-2000; 2000WO-US04342.
XX      PR      23-JUN-1999; 99US-0141037.
XX      PR      20-JUL-1999; 99US-0144758.
XX      PR      26-JUL-1999; 99US-0145698.
XX      PR      01-SEP-1999; 99WO-US20111.
XX      PR      29-OCT-1999; 99US-0162506.
XX      PR      30-NOV-1999; 99WO-US28313.
XX      PR      02-DEC-1999; 99WO-US28551.

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PR      16-DEC-1999; 99WO-US30095.
PR      05-JAN-2000; 2000WO-US00219.
PR      06-JAN-2000; 2000WO-US00376.
XX      XX
XX      PA      (GENTH ) GENENTECH INC.
PI      Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI      Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI      Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
PI      Watanabe CK, Williams PM, Wood WI;
XX      XX
XX      DR      WPI; 2001-071395/08.
PT      Secreted and transmembrane proteins and nucleic acids designated PRO,
PT      useful as hybridization probes, in chromosome and gene mapping and gene
PT      therapy -
PS      Claim 2; Fig 101; 787pp; English.
CC      The present invention relates to secreted and transmembrane proteins.
CC      These proteins and the DNA encoding them may be used as hybridization
CC      probes, in chromosome and gene mapping and in the generation of
CC      anti-sense RNA and DNA. They may also be used used to generate either
CC      transgenic animals or knockout animals which are in turn useful for
CC      development and screening of therapeutically useful reagents.
CC      The nucleic acids may also be used in gene therapy.
SQ      Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
XX      XX
Alignment Scores:
Pred. No.:      2 5e-122      Length:      1204
Score:      1523.00      Matches:      282
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels: 0
DB:      DB:      Gaps: 0

US-09-856-320A-2 (1-282) x AAF54320 (1-1204)
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Db      10 ATGCAGAGGTTGAGGTGGCTGCGGAGCTGGAAGTCATCGGGCAGAGGTCACAGCAGCC 69
QY      21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
Db      70 AAGAACTGGGGCCGCTCTCCCTCCAGGCCATGAGGATTCGCACTTAATCTG 129
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlnThrArgIleIleLysGlyPheGluCys 60
Db      130 CTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAAGATCATCAAGGGTTGAGTGC 189
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
Db      190 AAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTCCAGAAAGACGGGCTACTGTGGG 249
QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250 GCGAGCGTCATCGCCCCAGATGGCTCTGACACAGCCCACTCCCAACCCCGCTAC 309
QY      101 ILeValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysGlnGlnThrArgThr 120
Db      310 ATAGTTTCACTGGGGGAGCACAACCTCCAGAGAGAGAGGCTGTGAGCAGACCCGAGCA 369
QY      121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCCACTGAGTCTTCCCCCAGCCCGGCTTCAACAACAGCTCCCAACAAGAACACCGCC 429
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db      430 AATGACATCATCTGCTGTAAGATGGCATGCCAGTCTCCATCACCCTGGGCTGTGACCC 489
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180

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Db 490 CTCACCTCTCTCAGCTGTGTACTGTGTCAGCAGCAGCTGCTCATTTCCGGCTGGGC 549
 QY 181 SerThSerSerProGlnLeuAArgLeuProHisThrLeuArgCysAlaAenIleThrIle 200
 Db 550 AGCAGCTCCAGCCCCCAGTTACCGCTGCTCCTCACACCTTGGATGCGCCCAACATCACCATC 609
 QY 201 IleGlnHisGlnLysCysGlnAenAlaIleProGlnYasnIleThrAspThrMetValCys 220
 Db 610 ATTGACACACAGAGTGTGAGAACGCTTACCCCGGCAACATCAGACGACCATGGTGTGT 669
 QY 221 AlaSerValGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 240
 Db 670 GCCAGGCTGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 729
 QY 241 CysAsnGlnSerLeuGlnIleIleIleSerTrpGlnIleAspProCysAlaIleThrArg 260
 Db 730 TGTACCACTCTCTTCAAGGCAATTATCTCTGGGGCCAGGATCCGTGTGATCACCAG 789
 QY 261 LysProGlnValIleThrLysValCysGlyIleValIleAspTrpIleGlnIleThrMetLys 280
 Db 790 AAGCCTGTGTGTCTACAGCAAGCTCTCAATATATGTGATCGATCCAGGAGACGATGAG 849
 QY 281 AsnAsn 282
 Db 850 AACCAAT 855
 Db
 RESULT 8
 ABL95664
 ID ABL95664 standard; cDNA, 1204 BP.
 XX
 AC ABL95664;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human angiogenesis related cDNA PRO1279 SEQ ID NO: 207.
 XX
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnery;
 KM arteriosclerotic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US21735.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220644P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222659P.
 PR 17-AUG-2000; 2000WO-US23657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001US-0806666.
 PR 09-MAR-2001; 2001US-0802706.

PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.
 XX
 PA (GENT) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODOWSKI P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANJ) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P W.
 PA (WOOD) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PW, Wood WI, Ye W;
 PI WPI: 2002-171999/22.
 DR P-PSDB; ABB95526.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 1; Fig 207; 567pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention.
 CC
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 2,5e-122 Length: 1204
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-856-320A-2 (1-282) x ABL95664 (1-1204)
 QY 1 MetGlnArgLeuArgTrpLeuAArgAspTrpLysSerSerGlyArgGlyLeuThrAlaIle 20
 Db 10 ATGACAGAGTGTGAGTGTGCTGGGAGCTGGAAGTATCGGGAGAGGTCACACACACC 69
 QY 21 LysGlnProGlnValIleArgSerSerProLeuGlnAlaMetAlaGlnIleLeuGlnIleLeu 40
 Db 70 AAGGAACCTGGGCGCCGCTCTCCCTCCAGGCGCATGAGGATTCGACGTATCTCTG 129

QY 41 LeuAlaLeuAlaThGlyLeuValGlyGlyGlyLeuThrArgIleIleGlyGlyPheGlyCys 60
 Db 130 CTGGCTCTGGCAACAGGCGCTTGTAGGGGAGAGACAGATCATCAAGGGGTTCCAGTGC 189
 QY 61 LysProHisSerGlnProTrpGlnAlaLeuPheGlnLysThrArgLeuLeuGlyCys 80
 Db 190 AAGCTCATCTCCAGCGCTGGCAGGCGAGCGCTTTCGAGAACGCCGCTACTCTGTGG 249
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 100
 Db 250 GCGAGCTCATCGCCCGCAGATGGCTCCGACAGACGCCACTGCTCAAGCGCCGCTAC 309
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyGlyGlyGlyGlyGlyGly 120
 Db 310 ATAGTTTCACCTGGGCGAGCAACCTCCAGAGAGAGAGGGCTGTAGAGAGACCGGAGA 369
 QY 121 AlaThrGlySerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 Db 370 GCCACTGAGTCTTCCCGCCAGCCCGGCTTCAACACAGCTCCCAACAAACACACCGC 429
 QY 141 AsnAspIleMetLeuValIleMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 Db 430 AATGACATCATCTGCTGTAAGATGGATCGCAGTCTCCATCATCCTGGGCTGTGACCC 489
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
 Db 490 CTCACCTCTCTCCAGCTGTGTCACTGTGCACACAGCTGTGCTCATTTCCCGCTGGGC 549
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisSerThrLeuArgCysAlaAsnIleThrIle 200
 Db 550 AGCAGCTCCAGCCCGCCAGTGTAGCGCTGCTCAGACCTTCGATGCGCCACATCCATC 609
 QY 201 IleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsnIleThrAspThrMetValCys 220
 Db 610 ATTGAGCAGCAGAGATGTGAGAACGCTACCCCGGCAATCATCAGACCATGTGGTGT 669
 QY 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
 Db 670 GCCACGTCGAGAGAGGGGAGAGAGCTCTCCAGGGGAGCTCCGGGGCCCTTGTGTC 729
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
 Db 730 TGTATCCACTCTCTTCAAGCGATTATCTCTGGGCGCAGATCCGTGTGCCATCCCGA 789
 QY 261 LysProGlyValTrpThrLysValCysLysTrpValAspTrpIleGlnGlnThrMetLys 280
 Db 790 AAGCTGTGTGTACACAGAAAGTGTCAAAATATGTGACTGGATCCAGAGACGATGAAG 849
 QY 281 AsnAsn 282
 Db 850 AACCAAT 855
 Db 850 AACCAAT 855
 RESULT 9
 ABL88175
 ID ABL88175 standard; cDNA, 1204 BP.
 AC ABL88175;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO1279 cDNA sequence SEQ ID NO:207.
 XX
 XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
 KM vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KM angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KM age-related macular degeneration; arterial restenosis; angina;
 KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KM wound healing; chromosome mapping; gene mapping; gene; ss.
 XX
 OS Homo sapiens.
 XX

PN W0200200650-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US19692.
 XX
 PR 23-JUN-2000; 2000US-213637P.
 PR 20-JUL-2000; 2000US-213556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 XX
 PA (GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A;
 PI Godowski PJ, Gurney AJ, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2002-090516/12.
 DR P-PSDB; ABB84920.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 2; Fig 207; 565pp; English.
 XX
 AB ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytosolic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 XX
 SO Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:

Pred. No.: 2,5e-122 Length: 1204
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-856-320A-2 (1-282) x ABK3628 (1-1204)

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QY 21 LysGluProGlyValAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu
DB 70 AAGGAACCTGGGGCCGCTCTCTCCCTCCAGGCGCATGAGATTCTGCAATTATCTCTG
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGlyCys
DB 130 CTTCCTCTGGCAACAGGCTTGTAGGGGAGAGACCAAGATCATCAAGGGGTTCCAGTCC
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyIleThrArgLeuLeuCysGly
DB 190 AAGCTCAGCTCCAGGCTGAGCGAGCCCTGTCGAGAAAGACGGGCTACTCTGTGG
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTr
DB 250 GGCACGCTATGCGCCCGATGGCTCCGACAGCGCCAGCTCCTCAAGCCCGCTTAC
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlyGlnThrArgTr
DB 310 ATAGTTACACTGGGGAGAGACCAACCTCCAGGAAGAGAGGGCTGTAGACAGACCGGACA
QY 121 AlaThrGlnSerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg
DB 370 GGCAGTGAAGTCTTCCCGCCAGCCGCTTCAACAAAGAGCTCCCGCAACAAAGCCAGCCG
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro
DB 430 AATGACATCATCTGTGTGAAGATGGCATGCGCATCTCATCACTCGGCTGTGGACCC
QY 161 LeuThrLysSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly
DB 490 CTCACCCCTCTCTCAGCTGTGTCTACTGCTGGACCAAGCTGCTCTATTTCCGCTGGGAC
QY 181 SerThrSerSerProGlnLeuArgLeuProHisIleThrLeuArgCysAlaAsnIleThrIle
DB 550 AGCAGCTCCAGCCCGCAGTTAGCGCTGCGCTCACACCTTGCGATGGCCCAACATCACCATC
QY 201 IleGlnHisGlnLysGlyLysAsnAlaIleTrpGlyAsnIleThrAspThrMetValCys
DB 610 ATTGACACCAAGAGGTGAGAAAGCGCTTACCCCGGCAACATCAACAGACCAATGGTGT
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal
DB 670 GCCACGCTGCAAGAGGGGCAAGAGCTCTGCGCAGGGTACTCGGGGGCCCTCTGGTC
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg
DB 730 TGTAAACAGTCTCTTCAAGGATTAATCTCTGGGGGCAAGATCCGTTGCGATCACCCGA
QY 261 LysProGlyValIleThrLysValCysLysIleValAspTrpIleGlnGlnThrMetLys
DB 790 AAGCCGTGGTGTACACGAAGTGTGCAATATGTGACTGTGATCCAGAGAGCGATGAG
QY 281 AsnAsn 282
DB 850 AACCAAT 855
  
```

RESULT 10
ABK33628

```

ID ABK33628 standard; cDNA; 1204 BP.
AC ABK33628;
XX 08-MAY-2002 (first entry)
DT CDNA encoding human PRO protein, Seq ID No 185.
XX
DE
XX
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
XX
PR 25-JUL-2000; 2000US-220585P.
XX
PR 25-JUL-2000; 2000US-220605P.
XX
PR 25-JUL-2000; 2000US-220607P.
XX
PR 25-JUL-2000; 2000US-220624P.
XX
PR 25-JUL-2000; 2000US-220638P.
XX
PR 25-JUL-2000; 2000US-220664P.
XX
PR 25-JUL-2000; 2000US-220666P.
XX
PR 26-JUL-2000; 2000US-220893P.
XX
PR 28-JUL-2000; 2000WO-US20710.
XX
PR 23-AUG-2000; 2000WO-US23522.
XX
PR 24-AUG-2000; 2000WO-US23328.
XX
PR 15-SEP-2000; 2000US-000000P.
XX
PR 10-NOV-2000; 2000WO-US30873.
XX
PR 28-NOV-2000; 2000US-253646P.
XX
PR 01-DEC-2000; 2000WO-US33678.
XX
PR 20-DEC-2000; 2000US-0747259.
XX
PR 20-DEC-2000; 2000WO-US34956.
XX
PR 28-FEB-2001; 2000WO-US06520.
XX
PR 10-MAY-2001; 2001US-0854280.
XX
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GERTH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
DR WPI; 2002-172001/22.
XX
XX P-PSDB; AMU83684.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
XX
PS Claim 2; Figure 185; 359pp; English.
XX
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polypeptides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX and in chromosome and gene mapping. ABK33536-ABK33657 represent human
  
```

CC PRO protein coding sequences of the invention.

XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

SQ Alignment Scores:

Pred. No.:	2 5e-122	Length:	1204
Score:	1523.00	Matches:	282
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-856-320A-2 (1-282) x ABK33628 (1-1204)

```

QY 1 MetGlnArgLeuArgTyrPleuArgAspTyrPlySserSerGlyArgGlyLeuThrAlaAla 20
DB 10 ATGCAGAGGTGAGGTGCTGCGGAGCTGGAAGTCACTCGGCAGAGGTCTCAGACAGCC 69
QY 21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuLeu 40
DB 70 AAGGAACCTGGGCGCTCTCTCCCTCCAGGCCATGAGATTCTGCAATTAAATCTTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGlyCys 60
DB 130 CTTCCTCTGGCAACAGGCTTGTAGGGGAGAGACCAGATCATCAGGGCTTCAGATCC 189
QY 61 LysProHisSerGlnProTyrGlnAlaAlaLeuPheGlyLeuThrArgLeuLeuCysGly 80
DB 190 AAGCTCACTCCAGCCCTGGCAGGAGCCTGTTGAGAGACAGGGGCTACTGTGGG 249
QY 81 AlaThrLeuIleAlaProArgTyrPleuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGCTCATGCCCCAGATGCTCTCGACAGCAGCCCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlnGlyCysGlyGlnThrArgThr 120
DB 310 AATAGTTACCTGGGGAGCAACAACCTCCAGAAAGAGAGGGCTGTGAGAGACCCGGACA 369
QY 121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCACAGATGCTCTCCCCACCCCGCTTCAACAACAGCTCCCAACAAAGACACCGCC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrThrAlaValArgPro 160
DB 430 AATGACATCATCTGCTGAAGATGGCATCGCAGTCTCATCACTGGGCTGTGGACCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
DB 490 CTCACCTCTCTCAGCTGTCTCACTGCTGSCACCACTGCTCATTTCCGGCTGGGGC 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 550 AGCAGCTCAGCCCGCCAGTTACGCTGCTCCTCACACCTTGCATGCGCCAACTCACATC 609
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetAlaCys 220
DB 610 ATTGGACACCAAGATGTGAAGACCGCTACCCCGGACATACAGACACCAATGATGTTGT 669
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyLysAspSerGlyGlyProLeuVal 240
DB 670 GCCACGTCGACGAAAGGGGCAAGACTCTCTCCAGGGTGAATCCGGGGCCCTCTGGTTC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGlnAspProCysAlaIleThrArg 260
DB 730 TGTAAACAGTCTCTCAAGGCAATATCTCTGGGGCCAGAGATCCGTGTGCATCACCGGA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTyrIleGlnGlnThrMetLys 280
DB 790 AAGCTGTGTCTACACGAAGTGTGCAATATGTGACTGTGATCCAGAGACGATGAG 849
QY 281 AsnAsn 282
DB 850 AACCAAT 855

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RESULT 11
ID ACA03855
AC ACAA03855 standard; cDNA; 1204 BP.
XX
AC ACAA03855;
XX
DT 23-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #253.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumor necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytosolic; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PE 09-MAY-2002; 2002US-0143114.
XX
PF 31-MAR-1997; 97WO-US05230.
XX
PR 12-JUN-1998; 98WO-US12456.
XX
PR 14-JUL-1998; 98WO-US14552.
XX
PR 28-AUG-1998; 98WO-US17888.
XX
PR 10-SEP-1998; 98WO-US18824.
XX
PR 14-SEP-1998; 98WO-US19099.
XX
PR 14-SEP-1998; 98WO-US19099.
XX
PR 14-SEP-1998; 98WO-US19177.
XX
PR 16-SEP-1998; 98WO-US19330.
XX
PR 17-SEP-1998; 98WO-US19437.
XX
PR 07-OCT-1998; 98WO-US21141.
XX
PR 29-OCT-1998; 98WO-US22991.
XX
PR 29-OCT-1998; 98WO-US22992.
XX
PR 20-NOV-1998; 98WO-US24855.
XX
PR 01-DEC-1998; 98WO-US25108.
XX
PR 05-JAN-1999; 99WO-US00106.
XX
PR 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1999; 99WO-US05190.
XX
PR 20-APR-1999; 99WO-US08615.
XX
PR 14-MAY-1999; 99WO-US10733.
XX
PR 02-JUN-1999; 99WO-US12252.
XX
PR 01-SEP-1999; 99WO-US20111.
XX
PR 08-SEP-1999; 99WO-US20594.
XX
PR 13-SEP-1999; 99WO-US20944.
XX
PR 15-SEP-1999; 99WO-US21090.
XX
PR 15-SEP-1999; 99WO-US21547.
XX
PR 05-OCT-1999; 99WO-US23089.
XX
PR 29-NOV-1999; 99WO-US28214.
XX
PR 30-NOV-1999; 99WO-US28313.
XX
PR 30-NOV-1999; 99WO-US28409.
XX
PR 01-DEC-1999; 99WO-US28301.
XX
PR 02-DEC-1999; 99WO-US28634.
XX
PR 02-DEC-1999; 99WO-US28551.
XX
PR 02-DEC-1999; 99WO-US28564.
XX
PR 16-DEC-1999; 99WO-US28565.
XX
PR 16-DEC-1999; 99WO-US30095.
XX
PR 20-DEC-1999; 99WO-US30911.
XX
PR 20-DEC-1999; 99WO-US30999.
XX
PR 22-DEC-1999; 99WO-US30720.
XX
PR 30-DEC-1999; 99WO-US31274.
XX
PR 05-JAN-2000; 2000WO-US00219.
XX
PR 06-JAN-2000; 2000WO-US00277.
XX
PR 06-JAN-2000; 2000WO-US00376.
XX
PR 11-FEB-2000; 2000WO-US03565.
XX
PR 18-FEB-2000; 2000WO-US04341.
XX
PR 22-FEB-2000; 2000WO-US04414.
XX
PR 24-FEB-2000; 2000WO-US04914.

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24-FEB-2000; 2000MO-US05004.
 PR 01-MAR-2000; 2000MO-US05051.
 PR 02-MAR-2000; 2000MO-US05746.
 PR 02-MAR-2000; 2000MO-US05841.
 PR 10-MAR-2000; 2000MO-US06319.
 PR 15-MAR-2000; 2000MO-US06884.
 PR 20-MAR-2000; 2000MO-US07377.
 PR 21-MAR-2000; 2000MO-US07532.
 PR 30-MAR-2000; 2000MO-US08439.
 PR 17-MAY-2000; 2000MO-US13705.
 PR 22-MAY-2000; 2000MO-US14042.
 PR 30-MAY-2000; 2000MO-US14941.
 PR 02-JUN-2000; 2000MO-US15264.
 PR 28-JUL-2000; 2000MO-US20710.
 PR 11-AUG-2000; 2000MO-US22031.
 PR 23-AUG-2000; 2000MO-US23522.
 PR 24-AUG-2000; 2000MO-US23528.
 PR 08-NOV-2000; 2000MO-US30952.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 01-DEC-2000; 2000MO-US32678.
 PR 20-DEC-2000; 2000MO-US34956.
 PR 28-FEB-2001; 2001MO-US06520.
 PR 01-MAR-2001; 2001MO-US06666.
 PR 25-MAY-2001; 2001MO-US17092.
 PR 01-JUN-2001; 2001MO-US17800.
 PR 20-JUN-2001; 2001MO-US19692.
 PR 22-JUN-2001; 2001MO-US20116.
 PR 29-JUN-2001; 2001MO-US21066.
 PR 09-JUL-2001; 2001MO-US21735.
 PR 20-DEC-2000; 2000MO-US21735.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854280.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-332040/31.
 DR P-PSDB; ABU66822.
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping as chromosome markers, in
 PT tissue typing, and in chromosome identification
 XX
 PS Claim 2: Fig 505; 660bp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.

CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. ACN03603;ACN03877 represent cDNAs
 CC encoding the human PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsideEntry.html.
 XX
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 Alignment Scores:
 Pred. No.: 2,5e-122 Length: 1204
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0
 US-09-856-320A-2 (1-282) x ACN03855 (1-1204)
 QY 1 MetGlnArgLeuArgTyrPheuArgAspTyrLysSerSerGlyArgGlyLeuThrAlaAla 20
 DB 10 ATGCAGAGAGTTGAGGTGCTGCGGAGATGGAAGTATGATGCGGAGAGTCTCACAGAGCC 69
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
 DB 70 AAGGAACCTGGGGCCCGCTCTCCCTCCAGGCGCAAGAGATTCGAGTTAAATCTG 129
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLeuGlyPheGlyCys 60
 DB 130 CTTCCTCTGGCAACAGGGGCTTAGGGAGAGACAGAGATCATCAAGGGTTCCAGTTC 189
 QY 61 LysProHisSerGlnProTyrGlnAlaAlaLeuPheGlyLysThrArgLeuLeuCysGly 80
 DB 190 AAGCTCTACCTCCAGCCCTGCGAGGAGCCCTGTCGAGAGACCCGCTACTCTGTGGG 249
 QY 81 AlaThrLeuIleAlaProArgTyrPheuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 250 GCGAGCTCATATGCCCCAGATGGCTCTGACAGAGCCCACTGCTCAAGCCCGCTAC 309
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120
 DB 310 ATAGTTCACTGGGGCAGACACACCTCCAGAAAGGAGGGCTGTGACAGACGCCGACA 369
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 370 GCCACTGAGTCTCTCCACCCCGGCTTCAACAACACCTCCCAACAAGACACACCGC 429
 QY 141 AsnAspIleMetLeuValIleMetAlaSerProValSerIleThrAlaValArgPro 160
 DB 430 AATGACATCATGCTGGTGAAGATGATGATGCGAGTCTCATCATCTGGGCTGTGGACC 489
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
 DB 490 CTCACCTCTCTCTCAGCTGTGTCTGCTGTCAGCTGCTGCTCATTTCCGGCTGGGGC 549
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 DB 550 AGCAGCTCCACCCCACTTACGCTGCTGCTACACCTTGCATGCGCAACATCACCATC 609
 QY 201 IleGluHisGlnLysCysGluAsnAlaIleTyrProGlyAsnIleThrAspThrMetValys 220
 DB 610 ATTGAGCACCAAGATGTGAGAAAGCTTACCCGGCAACATCACAGACCAATGATGTGT 669
 QY 221 AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
 DB 670 GCCAGCGTGCAGGAAGGGGGCAAGAGATCTCTGCCAGGGTGACTCCGGGGCTCTGTGTC 729

PR	20-DEC-1999;	99MO-US30911.
PR	20-DEC-1999;	99MO-US30999.
PR	22-DEC-1999;	99MO-US30720.
PR	30-DEC-1999;	99MO-US31243.
PR	30-DEC-1999;	99MO-US31274.
PR	05-JUN-2000;	2000MO-US00219.
PR	06-JAN-2000;	2000MO-US00376.
PR	11-FEB-2000;	2000MO-US03565.
PR	18-FEB-2000;	2000MO-US04341.
PR	18-FEB-2000;	2000MO-US04342.
PR	22-FEB-2000;	2000MO-US04914.
PR	24-FEB-2000;	2000MO-US04914.
PR	24-FEB-2000;	2000MO-US05004.
PR	01-MAR-2000;	2000MO-US05601.
PR	02-MAR-2000;	2000MO-US05746.
PR	02-MAR-2000;	2000MO-US05841.
PR	10-MAR-2000;	2000MO-US06119.
PR	15-MAR-2000;	2000MO-US06884.
PR	20-MAR-2000;	2000MO-US07377.
PR	21-MAR-2000;	2000MO-US07532.
PR	30-MAR-2000;	2000MO-US08439.
PR	17-MAY-2000;	2000MO-US13705.
PR	22-MAY-2000;	2000MO-US14042.
PR	30-MAY-2000;	2000MO-US14941.
PR	02-JUN-2000;	2000MO-US15264.
PR	28-JUL-2000;	2000MO-US20710.
PR	11-AUG-2000;	2000MO-US22031.
PR	23-AUG-2000;	2000MO-US23522.
PR	24-AUG-2000;	2000MO-US23328.
PR	08-NOV-2000;	2000MO-US30952.
PR	10-NOV-2000;	2000MO-US30873.
PR	01-DEC-2000;	2000MO-US32678.
PR	20-DEC-2000;	2000MO-US34956.
PR	28-FEB-2001;	2001MO-US06520.
PR	01-MAR-2001;	2001MO-US06666.
PR	25-MAY-2001;	2001MO-US17092.
PR	01-JUN-2001;	2001MO-US17800.
PR	20-JUN-2001;	2001MO-US19692.
PR	22-JUN-2001;	2001MO-US20116.
PR	29-JUN-2001;	2001MO-US21066.
PR	09-JUL-2001;	2001MO-US21335.
PR	20-DEC-2000;	2000US-0747259.
PR	28-FEB-2001;	2001US-0796498.
PR	09-MAR-2001;	2001US-0802706.
PR	14-MAR-2001;	2001US-0808689.
PR	22-MAR-2001;	2001US-0816744.
PR	05-APR-2001;	2001US-0828366.
PR	10-MAY-2001;	2001US-0854208.
PR	10-MAY-2001;	2001US-0854280.
PR	18-MAY-2001;	2001US-0860716.
PR	25-MAY-2001;	2001US-0866028.
PR	25-MAY-2001;	2001US-0866034.
PR	01-JUN-2001;	2001US-0872035.
PR	05-JUN-2001;	2001US-0874503.
PR	14-JUN-2001;	2001US-0882636.
PR	19-JUN-2001;	2001US-0886342.
PR	21-JUN-2001;	2001US-0887879.
PR	18-JUL-2001;	2001US-0908827.
PR	06-AUG-2001;	2001US-0924419.
PR	09-AUG-2001;	2001US-0927796.
PR	16-AUG-2001;	2001US-0931836.
PR	19-DEC-2001;	2001US-0028072.
XX		
XX	(GETH) GENENTECH INC.	
XX		
PI	Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W	
PI	Gerlitsen M, Goddard A, Godowski PJ, Gunney AL, Sherwood S;	
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;	
XX	WPI, 2003-331925/31.	
XX	P-PSDB; ABU67098.	
XX		

PT New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer

PS Claim 2; Fig 505; 659pp; English.

XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumor necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the release or
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumor in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridization
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence encodes a PRO protein of the invention.

XX
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:

Pred. No.: 2,5e-122 Length: 1204
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0

US-09-856-320A-2 (1-282) x ACA04276 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
 DB 10 ATGCAAGAGTTAGAGGCTGGCGGACTGGAAGTCACTCCGGCAGAGCTTCACAGAGCC 69
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
 DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCCATAGAGTTTGTGAGTTAATCTTG 129
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGlyCys 60
 DB 130 CTGTGCTGTGGCAACAGGCTGTAGGGGAGAGACCATCATCAAGGGTTCCAGTGC 189
 QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
 DB 190 AAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTGCAAAACGCGGCTACTCTGTGG 249
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 250 GGCAGCCTATGCGCCCGCCAGATGGCTCTCGACAGACAGCCCATCTGCTCAAGCCCGCTAC 309
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlnGlnThrArgThr 120
 DB 310 ATAGTTCACTGGGGGAGCACAACCTCCAGAGAGAGAGGCTGTGTAGCAGACCGGAGACA 369

QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 370 GCCACTGAGTCTCTTCCCCACCCCGCTTCAACACAGCTCTCCCAACAAGACCCCGC 429
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 DB 430 AATGACATATCTGTTGTAAGATGGCATGCCAGTCTCATCATCCTGGGCTGTGGACCC 489
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
 DB 490 CTCACCTCTCTCCACGCTGTCTCACTGTCGACACCATGCTCTCATTTCCGCTGGGCG 549
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisIleThrLeuArgCysAlaAsnIleThrIle 200
 DB 550 ACACAGTCACGCCCCCAGTTAGCCTGCTTCAACCTTCGATGGCCCAACATCACCATT 609
 QY 201 IleGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
 DB 610 ATTGAGCACCACAAGTGTAGAACCGCTTACCCCGGACATCATCAGACACCATGCTGTGT 669
 QY 221 AlaSerValGlnGlyGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
 DB 670 GCAGGCTGCAGAGAGGGGCAAGACTCTCTCCAGGGTGACTCCGGGGCCCTCTGTC 729
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlnAspProCysAlaIleThrArg 260
 DB 730 TTTAACCACTCTCTTCAAGCATTTATCTCTGGGCGACAGATTCGTGTGATCACCCTCA 789
 QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
 DB 790 AAGCTCGGTGTACACGAACTCGCAATATGTGGACTGTGATCCAGAGACGATGAAG 849
 QY 281 AsnAsn 282
 DB 850 AACCAAT 855

RESULT 13
 ID ABX89393 standard; cDNA; 1204 BP.
 AC ABX89393;
 DT 13-MAY-2003 (first entry)
 XX
 XX
 DE DNA encoding novel secreted and transmembrane protein PRO1279.
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumor; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
 XX Homo sapiens.
 OS
 PN
 XX
 XX
 PD 23-JAN-2003.
 XX
 PF 07-MAY-2002; 2002US-0140808.
 XX
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.

Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0
 US-09-856-320A-2 (1-282) x ABX89393 (1-1204)

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QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgLLeuGlnLeuLLeu 40
DB 70 AAGGAACCTGGGGCCGCTCTCTCCCTCCAGGCAATGAGATTCGAGTTAATCTTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgLLeuLysGlyPheGlyCys 60
DB 130 CTTCCTCTGGCAGACAGGCTTTGAGGGAGAGACCAAGATCAAGAGGATTCGAGTCC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuCysGly 80
DB 190 AAGCCTCACTCCAGCCTGGCAGGAGCCCTGTTGAGAGAGCCGGCTACTCTGTGG 249
QY 81 AlaThrLeuLLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGCCTCATCGCCCCAGATGGCTCTGACAGCAGCCACCTGCTCAAGCCCCCTAC 309
QY 101 LLeuAlaHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyGlyGlyGlyGlyGlyGly 120
DB 310 ATAGTTCACTGGGAGACACACCTCCAGAGAGAGAGGAGGCTGTGAGAGACCGGACA 369
QY 121 AlaThrGlySerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GGCAGTGAAGTCTCTCCCAACCCCGGCTTCAACAAGAGTCTCCCAACAAGAGCAGCC 429
QY 141 AsnAspLLeuMetLeuValLysMetAlaSerProValSerLLeuThrTrpAlaValArgPro 160
DB 430 AATGACATCATCTGTGTGAAGATGGCATGCCAGTCTCCATGACCTGGGCTGTGAGACC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLLeuLysGlyTrpGly 180
DB 490 CTCACCTCTCTCAGAGTGTGTGACATGCTGGACACAGTCTGCTCATTTCCGGCTGGGG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnLLeuThrLLe 200
DB 550 AACAGCTCCAGCCCAAGTACAGCTGCTGCTCAGCCTTCCATGCGCCCAACATCACCATC 609
QY 201 LLeuGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnLLeuThrAspThrMetValCys 220
DB 610 ATTTGAGCACAGAAAGTGTAGAAAGCGCTACCCCGGCAACATCACAGACACCATGTGTGT 669
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
DB 670 GCCAGGCTCAGAGAAAGGGGCAAGAGCTCTCTCAGGAGGAGCTCCGGGGGCTCTGTGTC 729
QY 241 CysAsnGlnSerLeuGlnGlyLLeuLLeuSerTrpGlyGlnAspProCysAlaLLeuThrArg 260
DB 720 TGTAAACAGTCTCTCAAGGCAATTAATCTCTGGGGCAGAGATCCGTTGCCATCACCCGA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpLLeuGlnLLeuThrMetLys 280
DB 790 AAGCCTGTGTCTACAGCAAAAGTGTGAAATGTGAGTGTGATCCAGAGAGACATGAAG 849
QY 281 AsnAsn 282
DB 850 AACCAAT 855
  
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RESULT 14
 ID AAA61763
 AC AAA61763;
 XX
 XX
 DT 23-OCT-2000 (first entry)

DE CDNA encoding human serine protease BSSP6 (hBSSP6) SEQ ID NO.1.
 XX BSSP6; serine protease; human; hBSSP6; mouse; mBSSP6; brain;
 KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
 KW epilepsy; cancer; inflammation; infertility; pancreatitis;
 KW prostatic hypertrophy; ss.
 OS Homo sapiens.
 XX
 PN WO200031257-A1.
 XX
 XX 02-JUN-2000.
 XX
 PF 19-NOV-1999; 99WO-UP06476.
 XX
 PR 20-NOV-1998; 98UP-0347802.
 XX
 PA (FUSO) FUSO PHARM IND LTD.
 XX
 PI Uemura H, Okui A, Kominami K, Yamaguchi N, Mitsui S;
 DR WPI; 2000-40067/34.
 DR P-PSDB; AAB11712.
 XX
 PT Serine protease BSSP6, useful in detecting homologs, mutants and
 PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
 PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
 PT using blood or other tissues
 XX
 PS Claim 2; Page 67-69; 94pp; Japanese.
 XX
 CC The invention relates to novel serine proteases designated BSSP6
 CC (AAB11712-B11714), and to nucleic acids encoding them (AAA61763-A61765).
 CC The invention also relates to vectors and transformants comprising BSSP6
 CC nucleic acids; transgenic animals in which the expression level of BSSP6
 CC can be varied; and an mBSSP6 knockout mouse. The invention additionally
 CC encompasses anti-BSSP6 antibodies and methods of production of such
 CC antibodies; methods of BSSP6 detection using the antibodies, and the
 CC use of BSSP6 proteins or fragments as diagnostic markers for certain
 CC medical conditions. Nucleotides encoding BSSP6 were initially
 CC isolated in a human brain CDNA library using degenerate PCR primers
 CC (AAA61795-A61796) based on conserved regions of serine proteases. The
 CC BSSP6 serine proteases and nucleotides encoding them are useful in
 CC detecting homologues, mutants and polymorphic variants in biological
 CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
 CC and spleen) as diagnostic markers for conditions such as Alzheimer's
 CC disease, epilepsy, cancer, inflammation, infertility and prostatic
 CC hypertrophy. Sequences AAA61763 and AAA61765 represent cDNAs encoding
 CC human BSSP6 variants (hBSSP6) and sequence AAA61764 represents cDNA
 CC encoding murine BSSP6 (mBSSP6).
 XX
 SQ Sequence 1301 BP; 332 A; 387 C; 330 G; 252 T; 0 other;

Alignment Scores:
 Pred. No.: 2,766-122 Length: 1301
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-856-320A-2 (1-282) x AAA61763 (1-1301)

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QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyYArgGlyLeuThrAla 20
DB 113 ATGCAAGAGTTGAGTGGCTGGCGGACTGGAAGTCACTCCGGCAGAGTCTCACAGCAGCC 172
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgLLeuGlnLeuLLeu 40
DB 173 AAGGAACCTGGGGCCGCTCTCTCCCTCCAGGCAATGAGATTCGAGTTAATCTTG 232
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgLLeuLysGlyPheGlyCys 60
  
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Db      233 CTTCCTCTGCGCAACAGGCGCTTGAGGGGAGAGACCATGATCATCAAGGGGTTCCAGTCC 292
Qy      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuGly 80
Db      293 AAGCCTCACTCCAGGCGCTGGCAGGCGCCCTGTTGAGAGAGACGGCGCTACTCTGTGG 352
Qy      81 AlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 100
Db      353 GCGAGCGCTATCGCCCCGAGATGGCTCTCGACAGCGCCCGCTGCTCAAGCGCCGCTAC 412
Qy      101 IleValHisLeuGluGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgTrp 120
Db      413 ATAGTTCACTCGGCGAGACCAACCTCCAGAGAGAGAGGGCTGTAGACAGACCGGACA 472
Qy      121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      473 GCGACTGAGTCTCTCCCCACCCCGGCTTCAACAACAGCGCTCCCAACAAGACCCGCTAC 532
Qy      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db      533 AATGACATCATCTGATGAGATGCGATGCGCATGCTCCATCATCGGGCTGTGCGACCC 592
Qy      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLysSerGlyTrpGly 180
Db      593 CTCACCCCTCTCTCAAGCTGTGTCACTGCTGGCACCAAGCTGCTCATTTCCGGCTGGGCG 652
Qy      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      653 ACGACGTCAGAGCCCGCAGTTACGCCCTGCTCACACCTTCGATGCGCCAAACATCACATC 712
Qy      201 IlegLHisGlnLysGlnLysAsnAlaTrpProGlyAsnIleThrAspThrMetValCys 220
Db      713 ATTTGAGCACCAAGATGAGAAAGCGCTACCCCGGACATACACAGACACCATGGTGCT 772
Qy      221 AlaSerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
Db      773 GCGAGCGTCCAGGAAGGGGCAAGACCTCTCCAGGCGTACTCCGGGGCCCTCTGGTC 832
Qy      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db      833 TGTAAACAGACTCTCTCAAGGCAATTACTCTCGGGGCGAGATCCGCTGCGATCACCCGA 892
Qy      261 LysProGlyValThrThrLysValCysLysTrpValAspTrpIleGlnIleThrMetLys 280
Db      893 AAGCCTGGTGTACACGAAGCTGCATAATATGTGACTGATCCAGAGACGATGAAG 952
Qy      281 AsnAsn 282
Db      953 AACAAAT 958

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RESULT 15

AAZ30222
ID AAZ30222 standard; cDNA; 1314 BP.

AAZ30222;

11-FEB-2000 (first entry)

CDNA encoding a human prostate-associated serum protease (PRASP).

Human; prostate-associated serum protease; PRASP; neuropsin; PSA, abnormal prostate production; infertility; tubal disease; abnormal defect; endometriosis; polycystic ovary syndrome; autoimmune disorder; ectopic pregnancy; breast cancer; abnormal spermatogenesis; testicular cancer; adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 128..976
FT /tag= a
FT

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FT      FT      /product= "prostate-associated serum protease"
FT      misc_feature
FT      146..181
FT      /tag= b
FT      /note= "these nucleotides are separately claimed
FT      under claim 10"
FT      misc_feature
FT      344..382
FT      /tag= c
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FT      misc_feature
FT      551..589
FT      /tag= d
FT      /note= "these nucleotides are separately claimed
FT      under claim 10"
FT      WO9941387-A2.
FT      19-AUG-1999.
FT      05-FEB-1999; 99WO-US02571.
FT      17-FEB-1998; 98US-0025059.
FT      (INCY-) INCYTE PHARM INC.
FT      Tang YT, Corley NC, Guegler KJ;
FT      WPI; 2000-012993/01.
FT      P-PSDB; AAY43636.
FT      New prostate-associated serum protease and polynucleotides which
FT      identify and encode PRASP, useful for treating reproductive disorders
FT      and cancer.
FT      Claim 7; Fig 1A-D; 67pp; English.
FT      PS
FT      The present sequence encodes a human prostate-associated serum protease
FT      (PRASP). The protein shows homology to neuropsin, a brain-specific
FT      protease in mice, and PSA, a prostate-specific protease in humans.
FT      CC Nucleic acids encoding PRASP were first identified in Incyte clone
FT      CC 2723646 from the lung tumour cDNA library. Pharmaceutical compositions
FT      CC containing PRASP, or antibodies to PRASP, and mimetics, agonists,
FT      CC antagonists or inhibitors of PRASP, are used for treating or preventing
FT      CC a reproductive disorder or cancer. Examples of reproductive disorder
FT      CC include, abnormal prolactin production, infertility, tubal disease,
FT      CC ovulatory defects, endometriosis, polycystic ovary syndrome, autoimmune
FT      CC disorders, ectopic pregnancy, breast cancer, abnormal spermatogenesis
FT      CC and testicular cancer. Examples of cancers which may be treated or
FT      CC prevented include adenocarcinoma, leukemia, melanoma, myeloma,
FT      CC sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder,
FT      CC bone, bone marrow, brain, breast, cervix, penis, prostate, salivary
FT      CC glands, skin, spleen, testis, thymus, thyroid and uterus. A vector
FT      CC capable of expressing PRASP or an agonist which modulates the activity of
FT      CC PRASP may be administered to treat or prevent a reproductive disorder or
FT      CC cancer.
FT      XX
FT      SQ Sequence 1314 BP; 320 A; 400 C; 337 G; 257 T; 0 other.

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Alignment Scores:

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Query Match: 100.00% Indels: 0
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US-09-856-320A-2 (1-282) x AAZ30222 (1-1314)

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Qy      21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40

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Db 188 AAGAACTGGGGCCGCTCTCCCTCCAGCCATGAGATTCGCAATTATCTG 247
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleValGlyPheGlyCys 60
Db 248 CTGGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAAGATCATCAAGGGGTTCCAGTGC 307
QY 61 LysProHisSerGlnProTyrGlnAlaAlaLeuPheGlyLysThrArgLeuLeuGly 80
Db 308 AAGCTCACCCTCCAGCCCTGGCAGCAGCCCTGTCGAGAAAGCGCGCTACTCTGGG 367
QY 81 AlaThrLeuIleAlaProArgTyrPheLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db 368 GCGAGCCTCATCGCCCAAGATGCTCTGACAGACCCCATCGCTCAAGCCCGCTAC 427
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlyGlnThrArgThr 120
Db 428 ATAGTTCACCTGGGAGACCAACCTCCAGAGAGAGAGGGCTGTGAGACAGACCGGACA 487
QY 121 AlaThrGlySerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db 488 GCCACTGAGTCTTCCCGCCACCCCGCTTCAACACAGCCTCCCAACAAAGACACCGC 547
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTyrAlaValArgPro 160
Db 548 AATGACATCATGCTGTGAAGATGCGATCGCCAGTCTCCATCATCGGCTGTGCGACCC 607
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
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QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
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QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
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QY 281 AsnAsn 282
Db 968 AACAAAT 973

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Job time : 323.145 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 23, 2003, 15:49:25 ; Search time 309.593 Seconds

(without alignments)
2442.781 Million cell updates/sec

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Perfect score: 1523

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Ygapop 10.0 , Ygapext 0.5
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	1523	100.0	1204	11	US-09-946-374-169 Sequence 169, App
3	1523	100.0	1204	12	US-10-015-387A-169 Sequence 169, App
4	1523	100.0	1204	12	US-10-137-870-505 Sequence 505, App
5	1523	100.0	1204	12	US-10-140-018-505 Sequence 505, App
6	1523	100.0	1204	12	US-10-140-021-505 Sequence 505, App
7	1523	100.0	1204	12	US-10-140-274-505 Sequence 505, App
8	1523	100.0	1204	12	US-10-140-471-505 Sequence 505, App
9	1523	100.0	1204	12	US-10-140-807-505 Sequence 505, App
10	1523	100.0	1204	12	US-10-140-922-505 Sequence 505, App
11	1523	100.0	1204	12	US-10-140-924-505 Sequence 505, App
12	1523	100.0	1204	12	US-10-140-926-505 Sequence 505, App
13	1523	100.0	1204	12	US-10-141-698-505 Sequence 505, App
14	1523	100.0	1204	12	US-10-141-702-505 Sequence 505, App
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18	1523	100.0	1204	12	US-10-145-637-505 Sequence 505, App
19	1523	100.0	1204	12	US-10-145-698-505 Sequence 505, App
20	1523	100.0	1204	12	US-10-145-748-505 Sequence 505, App
21	1523	100.0	1204	12	US-10-145-823-505 Sequence 505, App
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23	1523	100.0	1204	12	US-10-145-870-505 Sequence 505, App
24	1523	100.0	1204	12	US-10-145-876-505 Sequence 505, App
25	1523	100.0	1204	12	US-10-145-959-505 Sequence 505, App
26	1523	100.0	1204	12	US-10-146-724-505 Sequence 505, App
27	1523	100.0	1204	12	US-10-146-725-505 Sequence 505, App
28	1523	100.0	1204	12	US-10-146-795-505 Sequence 505, App
29	1523	100.0	1204	12	US-10-147-501-505 Sequence 505, App
30	1523	100.0	1204	12	US-10-147-504-505 Sequence 505, App
31	1523	100.0	1204	12	US-10-147-506-505 Sequence 505, App
32	1523	100.0	1204	12	US-10-147-509-505 Sequence 505, App
33	1523	100.0	1204	12	US-10-147-511-505 Sequence 505, App
34	1523	100.0	1204	12	US-10-147-515-505 Sequence 505, App
35	1523	100.0	1204	12	US-10-147-529-505 Sequence 505, App
36	1523	100.0	1204	12	US-10-152-397-505 Sequence 505, App
37	1523	100.0	1204	12	US-10-153-586-505 Sequence 505, App
38	1523	100.0	1204	12	US-10-158-783-505 Sequence 505, App
39	1523	100.0	1204	12	US-10-158-786-505 Sequence 505, App
40	1523	100.0	1204	12	US-10-158-786-505 Sequence 505, App
41	1523	100.0	1204	12	US-10-158-786-505 Sequence 505, App
42	1523	100.0	1204	12	US-10-158-786-505 Sequence 505, App
43	1523	100.0	1204	12	US-10-158-786-505 Sequence 505, App
44	1523	100.0	1204	12	US-10-158-786-505 Sequence 505, App
45	1523	100.0	1204	12	US-10-158-786-505 Sequence 505, App

ALIGNMENTS

RESULT 1
US-10-205-823-211
; Sequence 211, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonesey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356

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; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-211

Alignment Scores:
Pred. No.: 5,08e-162 Length: 1186
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-205-823-211 (1-1186)

QY 1 MetGlnArgLeuArgTyrLeuArgApTyrPlySerSerGlyArgGlyLeuThrAlaAla 20
DB 26 ATGCAGAGGTTGAGGTGCTGCGGAGCTGGAAGTATCGGAGAGGTCTCACAGCAGCC 85
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
DB 86 AAGGAACCTGGGGCCCGCTCTCCCTCCAGGCGCATGAGATTCGAGTTAAATCCCG 145
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluTrnArgIleIleLysGlyPheGlyCys 60
DB 146 CTGGCTCTGGCAACAGGGCTTGTAGGGGAGAGACAGAGATCATCAGGGTTCCAGTGC 205
QY 61 LysProHisSerGlnProTyrGlnAlaAlaLeuPheGlyLysThrArgLeuLeuGly 80
DB 206 AAGCTCTACCTCCACCCCTGCGAGGAGCGCTTTCGAGAACCCGCTACTCTGTGGG 265
QY 81 AlaThrIleuIleAlaProArgTyrLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 266 GCGAGCTTCATGCCCCCAGATGGCTCTTGACAGAGCCCTGCTCAGCCCGCTAC 325
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120
DB 326 ATAGTTCACTGGGGAGAGCAACCTCCAGAGAGAGAGGCTGTGAGAGACCCGAGCA 385
QY 121 AlaThrGluSerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 386 GCCACTGTAGTCTCTCCACCCCGCTTCAACCAAGCTCTCCCAACCAACACCAACCGC 445
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTyrAlaValArgPro 160
DB 446 AATGACATATCTCTGTGAAGATGCATGCCAGTCTCCATCACTGGGCTGTGGACCC 505
QY 161 LeuThrLysSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
DB 506 CTCACCTCTCTCTACGCTGTCTACTGCTGSCACACAGTGTCTATTTCCGGCTGGGG 565
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLysLeuArgCysAlaAsnIleThrIle 200
DB 566 AGCAGGTCCAGCCCCCAGTTACGCTGCTCCACACTTGCATGCGCAACATCCACATC 625
QY 201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
DB 626 ATTGACACCAAGATGTGAGAACCGCTTACCCCGGCAACATACAGAACCATGGTGTGT 685
QY 221 AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
DB 686 GCCACGTCGAGAGAGGGGGCAAGAGACTCTCTCCAGGGGTGACTCCGGGGGCTCTGTGTC 745

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QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTyrPglYlnaPProCysAlaIleThrArg 260
DB 746 TGTAAACGATCTCTTCAAGGAGATTATCTCTGGGAGCAGATCCGTGTGCATCACCCGA 805
QY 261 LysProGlyValIleThrLysValCysLysTyrValAspTyrIleGlnGluThrMetLys 280
DB 806 AAGCTGTGTCTTACACCAAAAGTCTGCAAAATATGTGACTGTGATCCAGAGACATGAG 865
QY 281 AsnAsn 282
DB 866 AACAAAT 871

RESULT 2
US-09-946-374-169
; Sequence 169, Application US/09946374
; Publication No. US20030073129A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099602
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099642
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099754
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099763
PRIOR FILING DATE: 1998-09-10

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PRIOR APPLICATION NUMBER:	60/09792
PRIOR FILING DATE:	1988-09-10
PRIOR APPLICATION NUMBER:	60/099808
PRIOR FILING DATE:	1988-09-10
PRIOR APPLICATION NUMBER:	60/099812
PRIOR FILING DATE:	1988-09-10
PRIOR APPLICATION NUMBER:	60/099815
PRIOR FILING DATE:	1988-09-10
PRIOR APPLICATION NUMBER:	60/099816
PRIOR FILING DATE:	1988-09-10
PRIOR APPLICATION NUMBER:	60/100388
PRIOR FILING DATE:	1988-09-15
PRIOR APPLICATION NUMBER:	60/100390
PRIOR FILING DATE:	1988-09-15
PRIOR APPLICATION NUMBER:	60/100584
PRIOR FILING DATE:	1988-09-16
PRIOR APPLICATION NUMBER:	60/100627
PRIOR FILING DATE:	1988-09-16
PRIOR APPLICATION NUMBER:	60/100641
PRIOR FILING DATE:	1988-09-16
PRIOR APPLICATION NUMBER:	60/100683
PRIOR FILING DATE:	1988-09-17
PRIOR APPLICATION NUMBER:	60/100684
PRIOR FILING DATE:	1988-09-17
PRIOR APPLICATION NUMBER:	60/100710
PRIOR FILING DATE:	1988-09-17
PRIOR APPLICATION NUMBER:	60/100711
PRIOR FILING DATE:	1988-09-17
PRIOR APPLICATION NUMBER:	60/100848
PRIOR FILING DATE:	1988-09-18
PRIOR APPLICATION NUMBER:	60/100849
PRIOR FILING DATE:	1988-09-18
PRIOR APPLICATION NUMBER:	60/100919
PRIOR FILING DATE:	1988-09-17
PRIOR APPLICATION NUMBER:	60/100930
PRIOR FILING DATE:	1988-09-17
PRIOR APPLICATION NUMBER:	60/101014
PRIOR FILING DATE:	1988-09-18
PRIOR APPLICATION NUMBER:	60/101068
PRIOR FILING DATE:	1988-09-18
PRIOR APPLICATION NUMBER:	60/101071
PRIOR FILING DATE:	1988-09-18
PRIOR APPLICATION NUMBER:	60/101279
PRIOR FILING DATE:	1988-09-22
PRIOR APPLICATION NUMBER:	60/101471
PRIOR FILING DATE:	1988-09-23
PRIOR APPLICATION NUMBER:	60/101472
PRIOR FILING DATE:	1988-09-23
PRIOR APPLICATION NUMBER:	60/101474
PRIOR FILING DATE:	1988-09-23
PRIOR APPLICATION NUMBER:	60/101475
PRIOR FILING DATE:	1988-09-23
PRIOR APPLICATION NUMBER:	60/101476
PRIOR FILING DATE:	1988-09-23
PRIOR APPLICATION NUMBER:	60/101741
PRIOR FILING DATE:	1988-09-24
PRIOR APPLICATION NUMBER:	60/101742
PRIOR FILING DATE:	1988-09-24
PRIOR APPLICATION NUMBER:	60/101743
PRIOR FILING DATE:	1988-09-24
PRIOR APPLICATION NUMBER:	60/101915
PRIOR FILING DATE:	1988-09-24
PRIOR APPLICATION NUMBER:	60/101916
PRIOR FILING DATE:	1988-09-24

PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/102207
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102240
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102307
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102330
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102331
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102484
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102571
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102684
PRIOR FILING DATE: 1998-10-01	PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01	PRIOR APPLICATION NUMBER: 60/102688
PRIOR FILING DATE: 1998-10-02	PRIOR APPLICATION NUMBER: 60/102955
PRIOR FILING DATE: 1998-10-02	PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06	PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103355
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103396
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103401
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06	PRIOR APPLICATION NUMBER: 60/103633
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103678
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/104257
PRIOR FILING DATE: 1998-10-14	PRIOR APPLICATION NUMBER: 60/104967
PRIOR FILING DATE: 1998-10-20	PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20	PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20	PRIOR APPLICATION NUMBER: 60/105104
PRIOR FILING DATE: 1998-10-21	PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22	PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22	PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26	PRIOR APPLICATION NUMBER: 60/105654
PRIOR FILING DATE: 1998-10-26	PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores:		
Pred. No.:	5.19e-162	Length: 1204
Score:	1523.00	Matches: 282
Percent Similarity:	100.00%	Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-856-320A-2 (1-282) x US-09-946-374-169 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAla 20
 Db 10 ATGCAGAGGTTGAGGTGGCTGGCGGCTGGAGTCAATCGGCGAGAGTCTTCACAGCAGCC 69
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
 Db 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGCCATAGAGATCTGCAATTATCTTG 129
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleLysGlyPheGlyCys 60
 Db 130 CTTCGCTCTGGCAACAGGGCTTGGAGGGGAGAGACAGGATCATCAAGGGGTTGAGTGC 189
 QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLysGly 80
 Db 190 AAGCTCTACCTCCAGCCCTGGCAGCGACGCTGTTCGAGAACAGCGGGCTACTCTGTGG 249
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 100
 Db 250 GCGAGCTTATCGCCCCCAGATGGCTCTTGCACAGAGCCCTGCTTCAAGCCCGCTAC 309
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlnGlyCysGluGlnThrArgThr 120
 Db 310 AATAGTTACACTGGGGAGCACAACCTCCAGAGAGAGAGGGGTGTGAGCAGACCCGGACA 369
 QY 121 AlaThrGluSerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 Db 370 GCCACTGAGTCTTCCCTCCAGCCCGGCTTCAACACAGCTTCCCAACAGACCAACCCGC 429
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 Db 430 AATGACATATGCTGTGAGATGGCATGCGATGCTTCATCACTGGGCTGTGGACCC 489
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
 Db 490 CTCACCTCTCTCCACGCTGTGTCACTGTGGCACAGCTGCTCATTTCCGGCTGGGGC 549
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 Db 550 AGCAGCTCCAGCCCGCAGTTACGCTGCTCCACCTTGGCATGGCCCAACATCAACATC 609
 QY 201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
 Db 610 ATTGAGCACCAAGATGTGAGAACGCTTACCCCGGCAACATCAACAGACCTAGTGTGT 669
 QY 221 AlaSerValGlnGluGlyLysLysAspSerCysGlnGlyAspSerGlyCysProLeuVal 240
 Db 670 GCCACGTCGACAGAGGGGGCAAGGACTCTCTCCAGGGTGACTCCGGGGGCCCTCTGGTC 729
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
 Db 730 TGTAACTCAAGTCTTCAAGGCAATTAATCTCTGGGGCAGAGATCCGTGTGCGATCAACCGA 789
 QY 261 LysProGlyValIleThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
 Db 790 AAGCTGTGTCTTACACGAAAGTCTGCATAATGTGACTGATCCAGAGACGATGANG 849
 QY 281 AsnAsn 282
 Db 850 AACAAAT 855

RESULT 3

US-10-015-387A-169
 ; Sequence 169, Application US/10015387A

; Publication No. US20030135034A1
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830P1C54
 ; CURRENT APPLICATION NUMBER: US/10/015,387A
 ; CURRENT FILING DATE: 2001-12-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 169
 ; LENGTH: 1204
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-015-387A-169

Alignment Scores:

Pred. No.: 5,19e-162 Length: 1204
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-015-387A-169 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAla 20
 Db 10 ATGCAGAGGTTGAGGTGGCTGGCGGCTGGAGTCAATCGGCGAGAGTCTTCACAGCAGCC 69
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
 Db 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGCCATAGAGATCTTCAAGGGGTTGAGTGC 129
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleLysGlyPheGlyCys 60
 Db 130 CTTCGCTCTGGCAACAGGGCTTGGAGGGGAGAGACAGGATCATCAAGGGGTTGAGTGC 189
 QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLysGly 80
 Db 190 AAGCTCTACCTCCAGCCCTGGCAGCGACGCTGTTCGAGAACAGCGGGCTACTCTGTGG 249
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 100
 Db 250 GCGAGCTTATCGCCCCCAGATGGCTCTTGCACAGAGCCCTGCTTCAAGCCCGCTAC 309
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlnGlyCysGluGlnThrArgThr 120
 Db 310 AATAGTTACACTGGGGAGCACAACCTCCAGAGAGAGAGGGGTGTGAGCAGACCCGGACA 369
 QY 121 AlaThrGluSerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 Db 370 GCCACTGAGTCTTCCCTCCAGCCCGGCTTCAACACAGCTTCCCAACAGACCAACCCGC 429
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 Db 430 AATGACATATGCTGTGAGATGGCATGCGATGCTTCATCACTGGGCTGTGGACCC 489
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
 Db 490 CTCACCTCTCTCCACGCTGTGTCACTGTGGCACAGCTGCTCATTTCCGGCTGGGGC 549
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200


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Db      550 AGCAGCTCCAGCCCGCCAGTTACGCTGCTCCTACACCTTGAGATGGCCAAACATCACCANTC 609
QY      201 ILeGluHISGlnIlyScysGluuAsnAlaTYrProGlyAsnIleThrsAspThrMetValCys 220
Db      610 ATTGACACACCAAGAGGTGTGAGAAAGCGCTACCCGGCAACCTCACAACACCATGAGTGTGT 669
QY      221 AlaSerValGlnGlnIlyGlyIlyAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
Db      670 GCCAGGCTGCAGAGAGGGGGCAAGACTCCTGCCAGGGTGACTCCGGGGCCCTCTGTGTCT 729
QY      241 CysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGlnAspProCysAlaIleThrArg 260
Db      730 TGTAAACAGCTCTCTTCAAGGCATTATCTCTGGGGCCAGGATCCGTGTGATCACCAGCA 789
QY      261 LysProGlyValIlyThrIlyAspValCysLysTyrValAspTropIleGlnGlnThrMetLys 280
Db      790 AACCTGTGGTGTCTACAGAAAGTCTCAAAATATGTGACTGATCCAGAGAGATGAAG 849
QY      281 AsnAsn 282
Db      850 AACAAAT 855

RESULT 4
US-10-137-870-505
; Sequence 505, Application US/10137870
; Publication No. US2003013883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C155
; CURRENT APPLICATION NUMBER: US/10/137,870
; PRIOR FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-870-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 12

US-09-856-320A-2 (1-282) x US-10-137-870-505 (1-1204)
QY      1 MetGlnArgLeuArgTyrPleuArgAspTyrLysSerSerGlyArgGlyLeuThrAlaAla 20
Db      10 ATGCAAGAGGTGTGAGGTGTGCGGGACTGGAAGTCTATCGGGAGAGGTCTTCACACAGGCC 69
QY      21 LysGluProGlyAlaIlySerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40

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Db      70 AAGGAACCTGGGGCCCGGCTCTCCCCCTCCAGGCCATGAGGATTCGTGAGTTAATCTCG 129
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIleThrArgIleIleLysGlyPheGlyCys 60
Db      130 CTGTGCTGGCAACAGGGCTTGTAGGGGAGAGACCATGATCATCAAGGGGTTCGATGCC 189
QY      61 LysProHisSerGlyProTyrGlnAlaIleAlaPheGlnLysThrArgLeuLeuCysGly 80
Db      190 AAGCTCTACTCCCAAGCCCTGGGACAGGAGCCCTGTTGAGAAAGCCGGCTACTCTGTGG 249
QY      81 AlaThrLeuIleAlaProArgTyrPleuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250 GCGAGCTCATGCGCCCGCCAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCGCTAC 309
QY      101 ILeValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyIlyCysGlyIleThrArgThr 120
Db      310 ATAGTTACCTGGGGACAGCAACCTCCAGAAAGGAGAGGGTGTGTAGAGACCCCGACA 369
QY      121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCCACTGAGTCTTCTCCCAACCCCGCTTCAACACAGCTCTCCCAACAAAGACACCCG 429
QY      141 AsnAspIleMetLeuValIlySerMetAlaSerProValSerIleThrTyrAlaValArgPro 160
Db      430 AATGACATCATGCTGTGTGAAGATGGCATGCGCAGTCTCATCATCAGCTGGGCTGTGGACCC 489
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
Db      490 CTCACCTCTCTCTCAAGCTGTGTCTCACTGCTGACACAGCTGCTCATTTCCGGCTGGGG 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550 AACAGCTGAGCCCGCCAGTTACGCTGCTCCTCACCTTGCGATGGCCAAACATCACCATC 609
QY      201 ILeGluHISGlnIlyScysGluuAsnAlaTYrProGlyAsnIleThrsAspThrMetValCys 220
Db      610 ATTGACACACCAAGAGGTGTGAGAAAGCGCTACCCGGCAACATCAGACACCATGAGTGT 669
QY      221 AlaSerValGlnGlnIlyGlyIlyAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
Db      670 GCCAGGCTGCAGAGAGGGGGCAAGACTCCTGCCAGGGTGACTCCGGGGCCCTCTGTGTCT 729
QY      241 CysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGlnAspProCysAlaIleThrArg 260
Db      730 TGTAAACAGCTCTCTTCAAGGCATTATCTCTGGGGCCAGGATCCGTGTGATCACCAGCA 789
QY      261 LysProGlyValIlyThrIlyAspValCysLysTyrValAspTropIleGlnGlnThrMetLys 280
Db      790 AAGCTGTGGTGTCTACAGAAAGTCTCAAAATATGTGACTGATCCAGAGAGATGAAG 849
QY      281 AsnAsn 282
Db      850 AACAAAT 855

RESULT 5
US-10-140-018-505
; Sequence 505, Application US/10140018
; Publication No. US2003013885A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

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; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-140-018-505 (1-1204)

Qy 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db 10 ATGCAGAGGTTCAGGTGCTGCGGAGCATGGAAGTATCATCGGAGAGTCTCACAGCAGCC 69
Qy 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgGlyLeuGlnLeuLeu 40
Db 70 AAGGAACTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCCTCAGTTAATCTGT 129
Qy 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgGlyLeuLeuGlyPheGluCys 60
Db 130 CTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACAGGATATCAAGGGGTTCAGATGC 189
Qy 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLeuThrArgLeuLeuGly 80
Db 190 AAGCTCACTCCCAAGCCCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 249
Qy 81 AlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysAspHisArg 100
Db 250 GCGAGCTCATGCGCCCGAGATGCTCTGACAGAGCCCACTGCTCAAGCCCGCTAC 309
Qy 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlyGlnThrArgThr 120
Db 310 ATAGTTCACTTGGGAGAGACCACTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 369
Qy 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db 370 GCCACTGAGTCTCTCCCGCCAGCCCGGCTTCAACACAGGCTCCCAACAAAGACCAAGCC 429
Qy 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db 430 AATGACATCATGCTGTGTGAAGATGGCATGCGCATCTCATCACTGGAGTGTGGAGCC 489
Qy 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db 490 CTCACCTCTCTCTCAGCTGTCTCTGCTGACCACTGCTCATATTCGGCGTGGGGC 549
Qy 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db 550 AGCAGCTCAGGCCCGCAGTTCAGCTGCTGCTACACTTGCATGGCCAAATCAGCATC 609
Qy 201 IleGluHisGlnLysCysGlyLysAsnAlaTrpProGlyAsnIleThrAspThrMetValCys 220
Db 610 ATTGGACCAAGAAAGTGTGAAGAACCTTACCCCGCAACATCAAGACACCATGTGTGT 669
Qy 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
Db 670 GCCACCTGACAGAGAGGGGCAAGGATCTCTGCGCAGGTTGACTCCGGGGGCTCTGTG 729

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Qy 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db 730 TGTAAACCGTCTCTTCAAGGATATATCTCCGGGGCCAGGATCCGTGTCATACCCGA 789
Qy 261 LysProGlyValIleThrTrpValCysLysTrpValAspTrpIleGlnGlyThrMetLys 280
Db 790 AAGCTGTGTCTACAGAAAGTCTGCAAAATGTGAGTGTGATTCAGAGACATGAG 849
Qy 281 AsnAsn 282
Db 850 AACAAAT 855

RESULT 6
US-10-140-021-505
; Sequence 505, Application US/10140021
; Publication No. US2003013886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-021-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-140-021-505 (1-1204)

Qy 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db 10 ATGCAGAGGTTCAGGTGCTGCGGAGCATGGAAGTATCATCGGAGAGTCTCACAGCAGCC 69
Qy 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgGlyLeuGlnLeuLeu 40
Db 70 AAGGAACTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCCTCAGTTAATCTGT 129
Qy 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgGlyLeuLeuGlyPheGluCys 60
Db 130 CTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACAGGATATCAAGGGGTTCAGATGC 189
Qy 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLeuThrArgLeuLeuGly 80
Db 190 AAGCTCACTCCCAAGCCCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 249

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QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250 GCGAGCCTCATGCCCGCCAGATGGCTCTCCAGCAGCAAGCCACCTCCAAAGCCCCCTAC 309
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlnGlyCysGlnGlnThrArgThr 120
Db      310 ATAGTTCACCTGGGAGAGCAACCTCCAGAAAGAGAGGGCTGTGAGCAGACCCGAGACA 369
QY      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCCACTGAGCTCTTCCCGCCAGCTTCCAAACAAAGAGCTCCCGCCAAAGAGCCACCCG 429
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db      430 AATGACATCATGTGTGTGAAGATGGCATGCCAGTCTCCATCCACTGGGCTGTGCGACCC 489
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db      490 CTCACCCCTCTCCTCAGCTGTGTCACTGTGGCAGCAGCTGCTATTTCCGGCTGGGG 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550 AGCAGCTCCAGCCCCCAGTTACGCCCTGCTCACACCTTGAGTGCCTCAACATCACCATC 609
QY      201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
Db      610 ATTGACACCAAGAGTGTAGAGAGCGCTTACCCCGGCAACATCACAACACCATGGTGT 669
QY      221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
Db      670 GCCAGCGTCCAGAAAGGGGCAAGAGACTCTGCGCAGGGTGAATCCGGGGGCCCTCGTGC 729
QY      241 CysAsnGlnSerLeuGlnGlnIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db      730 TGTAAACAGTCTCTTCAAGGCAATTACTCTGGGGCAGAGATCGTGTGCATGCCCA 789
QY      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
Db      790 AAGCTGTGTCTACACGAAAGTGTGCAATATGTGACTGATCCAGAGACGATGAAG 849
QY      281 AsnAsn 282
Db      850 AACAAAT 855

RESULT 7
US-10-140-274-505
; Sequence 505, Application US/10140274
; Publication No. US20030143674A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DePoyre, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C161
; CURRENT APPLICATION NUMBER: US/10/140,274
; PRIOR APPLICATION removed - See File Wrapper or Palm

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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-274-505

Alignment Scores:
Pred. No.: 5 19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-140-274-505 (1-1204)

QY      1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db      10 ATGCAAGAGTTAGAGTGGCTGGCGAGCTGGAAATCATCGGCGAGAGAGTCTCACAGACCC 69
QY      21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
Db      70 AAGCAACCTGGGGCCCGCTCTCCCGCTCCAGGCCATGAGAGATTCTGCAGTTAATCTTG 129
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlyTrpArgIleIleLysGlyPheGlyCys 60
Db      130 CTTGCTCTGGCAACAGGCTGTGTAGGGGAGAGACAGAGATATCAAGGGGTTTCAGTGC 189
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuCysGly 80
Db      190 AAGCTCTACTCCACAGCCCTGGCAGGAGGCCCTGTTCAGAGAACCCGGCTACTCTGTGG 249
QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250 GCGAGCGTCAATGCCCGCCAGATGGCTCTGACAGACGCCACTGCTCAAGCCCCGCTAC 309
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlnGlyCysGlnGlnThrArgThr 120
Db      310 ATAGTTCACCTGGGAGAGCAACCTCCAGAAAGAGAGGGCTGTGAGCAGACCCGAGACA 369
QY      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCCACTGAGTCTCTTCCCGCCAGCTTCCAAACAAAGCTTCCCAACAAAGACACCCG 429
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db      430 AATGACATCATGTGTGTGAAGATGGCATGCGCAGTCTCCATCAGCTGGGCTGTGCGACC 489
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db      490 CTCACCCCTCTCCTCAGCTGTGTCACTGTGGCAGACCACTGCTTATTTCCGGCTGGGG 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLysArgCysAlaAsnIleThrIle 200
Db      550 AGCAGCTCCAGCCCCCAGTTACGCTGCTCACACCTTGCGATGGGCCAACATCCACATC 609
QY      201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
Db      610 ATTGACACCAAGAGTGTGAAGACGCTTACCCCGGCAACATCAGACACCATGTGTGT 669
QY      221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
Db      670 GCCAGCGTCCAGAAAGGGGCAAGAGACTCTGCGCAGGGTGAATCCGGGGGCCCTGTGTC 729
QY      241 CysAsnGlnSerLeuGlnGlnIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db      730 TGTAAACAGTCTCTTCAAGGCAATTACTCTGGGGCAGAGATCCCTGTGCGATCCCGCA 789
QY      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
Db      790 AAGCTGTGTCTACACGAAAGTGTGCAATATGTGACTGATCCAGAGACGATGAAG 849

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QY 281 AsnAsn 282
 DB 850 AACAAAT 855

RESULT 8

US-10-140-471-505
 ; Sequence 505, Application US/10140471
 ; Publication No. US20030138887A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: Deforge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3330R1C163
 CURRENT APPLICATION NUMBER: US/10/140,471
 CURRENT FILING DATE: 2002-05-06
 Prior Application removed - See file wrapper or Palm
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 505
 LENGTH: 1204
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-140-471-505

Alignment Scores:

Pred. No.: 5,19e-162 Length: 1204
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-140-471-505 (1-1204)

QY 1 MetGlnAglLeuAgtTrrpLeuAgsptRplysSerSerGlyAargGlyLeuThraAla 20
 DB 10 ATGCAAGAGTTCAGGTGGCTGCGGAGCTGGAAGTATCGGCGAGAGTCTCACACAGCC 69
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
 DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGSCATGAGATTCTGAGTTAATCTG 129
 QY 41 LeuAlaLeuAlaThGlyLeuValGlyGlnThrArgIleIleLeuGlyPheGluCys 60
 DB 130 CTGCTCTGCGCAACAGGCTTGTAGGGGAGAGACAGCATATCAAGGGTTCAGTGC 189
 QY 61 LysProHisSerGlnProTrrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuGly 80
 DB 190 AAGCTCTACCTCCACCTGCGAGGAGCCCTGTTCTGAGAGACCGGCTACTCTGTGG 249
 QY 81 AlaThrLeuIleAlaProArgTrrpLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 250 GCGAGCTCATGCGCCCAAGATGGCTCTCTGACAGAGCCCACTGCTCAAGCCCGCTAC 309
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGluGlyCysGlnGlnThrArgThr 120
 DB 310 ATAGTTCACTCTGGCGAGACAACTCCAGAAAGAGAGGGGCTGTGAGAGACCCGGACA 369

QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 370 GCCACTGAGTCTTCCCTCCACCCGCGCTTCAACAAACACCTCCCAAAAGACACCGC 429
 QY 141 AsnAspIleMetLeuValIleMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 DB 430 AATGACATCATGCTGTGTGAAGATGGCATCGCAGTCTCCATCACCCTGGCTGTGGACCC 489
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrrpGly 180
 DB 490 CTCACCTCTCTCCTACCGCTGTGTCACTGTGGACACACCTGCTCATTTCCGGCTGGGCG 549
 QY 181 SerThrSerSerProGlnIleuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 DB 550 AGCAGCTCACCCCAAGTTAGCCTGCTTACACCTTGCGATGGCCCAACATCAACATC 609
 QY 201 IleGluHisGlnLysCysGluAsnAlaTrrpProGlyAsnIleThrAspThrMetValCys 220
 DB 610 ATTGACACCAAGAGTGTGAAGACCCCTACCCCGGCAACATCACAGACACCATGTGTGT 669
 QY 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlnLysAspSerGlyProLeuVal 240
 DB 670 GCCAGCTGACAGAAAGGGGCAAGACTCTGCCAGGAGTGACTCCGGGGCTCTGTGTC 729
 QY 241 CysAsnGlnSerLeuGlnGlnIleIleSerTrrpGlyGlnAspProCysAlaIleThrArg 260
 DB 730 TGTAACTGCTCTTCAAGGAGATTATCTCTGGGGCCAGAGTCCGTGCGATACACCGGA 789
 QY 261 LysProGlyValTrrpThrLeuValCysLysTrrpValAspTrrpIleGlnGluThrMetLys 280
 DB 790 AAGCTGTGTCTACACAGAAAGTCTGCMAATATGTGACTGATTCAGAGACATGAG 849

QY 281 AsnAsn 282
 DB 850 AACAAAT 855

RESULT 9

US-10-140-807-505
 ; Sequence 505, Application US/10140807
 ; Publication No. US20030134354A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: Deforge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3330R1C174
 CURRENT APPLICATION NUMBER: US/10/140,807
 CURRENT FILING DATE: 2002-05-07
 Prior Application removed - See file wrapper or Palm
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 505
 LENGTH: 1204
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-140-807-505

Alignment Scores:
 Pred. No.: 5,19e-162 Length: 1204

Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-09-856-320A-2 (1-282) x US-10-140-807-505 (1-1204)
QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSergIyAArgGlyLeuThrAlaAla 20
DB 10 ATGCAAGAGTTGAGTGGCTGGCGGAGCTGGAAGTCAATCGGAGAGGTCTCACAGACGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
DB 70 AAGGAACCTGGGGCCCGCTCTCCCTCCAGGCGATGAGATTCTGCAGTTAACTCG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIleThrArgIleIleLysGlyPheGlyCys 60
DB 130 CTGGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAAGATCATCAAGGGGTTGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
DB 190 AAGCTCTCACTCCAGCCCTGGCGAGGAGCCCTGTGTGAGAAGACGGGCTACTGTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GGGAGGCTCATGGCCCGCCAGATGGCTCTCGACAGACGCCACCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlyIleThrArgThr 120
DB 310 ATAGTTACACCTGGGGCGAGCAAACTCCAGAAAGAGAGGGGTGTGAGACAGCCGACA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACTGAGTCTTCCCTCCAGCCCGGCTTCAACAAAGCCCTCCCAACAAAGCCCGC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 430 AATGACATCATGTGTGTAAGATGGCATGGCCAGTCTCCATCACTGGGCTGTGCAACC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSergIyTrpGly 180
DB 490 CTCACCTCTCCCTCAGCGCTGTGCTGAGGACAGCGCTCATTTCCGGCTGGGCG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 550 AGACGCTCCAGCCCGCCAGTTACGCTGCTCACACCTTCGATGGCCCAACATCACCATC 609
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
DB 610 ATTGAGCACCAAGAGTGTAGAACGCTTACCCCGGCAACATCACAGACCATGTGTGT 669
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSergIyGlyProLeuVal 240
DB 670 GCCAGGCTCAGAGAGGGGGCAAGGACTCTGCGAGGCTGACTCGGGGGCCCTCGGTC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB 730 TTTAACCAATCTCTTCAAGGCAATTAATCTCTGGGGCAGAGATCCGTTGCGATCCCA 789
QY 261 LysProGlyValIleThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
DB 799 AAGCTCTGGTCTTACACGAAGTGTGCAATATGTGACTGGATCCAGAGACGATGAG 849
QY 281 AsnAsn 282
DB 850 AACCAAT 855
RESULT 10
US-10-140-922-505
; Sequence 505, Application US/10140922
; Publication No. US20030138889A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C179
CURRENT APPLICATION NUMBER: US/10/140,922
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See Palm or File wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-922-505
Alignment Scores:
Pred. No.: 5 196-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-09-856-320A-2 (1-282) x US-10-140-922-505 (1-1204)
QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSergIyAArgGlyLeuThrAlaAla 20
DB 10 ATGCAAGAGTTGAGTGGCTGGCGGAGCTGGAAGTCAATCGGAGAGGTCTCACAGACGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
DB 70 AAGGAACCTGGGGCCCGCTCTCCCTCCAGGCGCATGAGATTCTGCAGTTAACTCG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIleThrArgIleIleLysGlyPheGlyCys 60
DB 130 CTGGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAAGATCATCAAGGGGTTGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
DB 190 AAGCTCTCACTCCAGCCCTGGCGAGGAGCCCTGTGTGAGAAGACCGGCTACTGTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GGGAGGCTCATGGCCCGCCAGATGGCTCTCGACAGACGCCCTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlyIleThrArgThr 120
DB 310 ATAGTTACACCTGGGGCGAGCAAACTCCAGAAAGAGGGGTGTGAGACAGCCGACA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACTGAGTCTTCCCTCCAGCCCGGCTTCAACAAAGCCCTCCCAACAAAGCCCGC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 430 AATGACATCATGTGTGTAAGATGGCATGGCCAGTCTCCATCACTGGGCTGTGCAACC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSergIyTrpGly 180

```

Db      490 CTCACCTCTCTCTCAGCGTGTCTACTGTCGACACAGCTGCTTATTCGGCTGGGC 549
Qy      181 SerThrsSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550 AGCAGCTCCAGGCCCCAGTTAGCCTGCTGCTCACACCTTGCGATGGCCACATCCACATC 609
Qy      201 IleguHISGlnLysCysGlnAsnAlaTyProGlnAsnIleThrAspThrMetValCys 220
Db      610 ATTGAGCACACGAGAGTGTAGAACGCTCTCCCGGCAACATCACAGACCATGTGTGT 669
Qy      221 AlaSerValGlnGlnGlyGlyAspSerCysGlnGlnIleAspSerGlyGlyProLeuVal 240
Db      670 GCCACGTCGACGAAAGGGGGCAAGACTCTCTCCAGGGTACTCCGGGGGCTCTGTGTC 729
Qy      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlnAspProCysAlaIleThrArg 260
Db      730 TGTAAACAGTCTCTTCAAGGCAATTATCTCTGGGGCGAGATCCGTTGTCCGATCACCCGA 789
Qy      261 LysProGlyValTyThrIleValCysIleTyValAspTrpIleGlnIleThrMetLys 280
Db      790 AAGCTGTGTGTCTACACGAAAGCTGTGCAAAATATGTGACTGTGATCCAGAGACGATGAAG 849
Qy      281 AsnAsn 282
Db      850 AACCAAT 855

```

RESULT 11

US-10-140-924-505

; Sequence 505, Application US/10140924

; Publication No. US2003013435A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C177

; CURRENT APPLICATION NUMBER: US/10/140,924

; PRIORITY FILING DATE: 2002-05-07

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 505

; LENGTH: 1204

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-140-924-505

Alignment Scores:

Pred. No.: 5,19e-162

Score: 1523.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

Length: 1204

Matches: 282

Conservative: 0

Mismatch: 0

Indels: 0

Gaps: 0

US-09-856-320A-2 (1-282) x US-10-140-924-505 (1-1204)

Qy 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaIle 20

```

Db      10 ATGAGAGGTTGAGGTGCTCGGAGCTGAAAGTCATGGGCAAGAGCTTACAGCACCC 69
Qy      21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
Db      70 AAGGAACTGGGGCCCGCTCTCTCCCTCCAGGCCATGAGAGATTGTGCAATTATCTGT 129
Qy      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLeuGlyPheGlyCys 60
Db      130 CTGTGTCGCAACAGGCGCTGTAGGGGAGAGACACAGATCATCAAGGGGTTCCAGTGC 189
Qy      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysTrpArgLeuLeuCysGly 80
Db      190 AAGCTCACTCCAGCCCTGAGAGACAGCCCTGTTCGAAAGACGGGCTACTCTGTGG 249
Qy      81 AlaThrLeuAlaAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTy 100
Db      250 GCGAGCGTCATCGCCCCAGATGGCTCTGACAGAGCCCACTGCTCAAGCCCGCTAC 309
Qy      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyGlyGlnThrArgThr 120
Db      310 ATAGTTCACTGGGGCAGACACACCTCCAGAGAGGAGGGGCTGTGACACACCCGACA 369
Qy      121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCCACTGATCTCTCCACCCTCCGCTTCAACAACAGCTCCCAACAAGACACACCGC 429
Qy      141 AsnAspIleMetLeuValSerIleMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db      430 AATGACATCATCTGTGTGAATGATGGATCGCAGTCTCCATCAGCTGGGCTGTGGACCC 489
Qy      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db      490 CTCACCTCTCTCTCAGCTGTGTCACTGTGACACAGCTCCATATTCGGGCTGGGGC 549
Qy      181 SerThrsSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550 AGCAGCTCACGCCCCCAATTAGCCTGCTTACACCTTGCCATGGGCAACATCACCATC 609
Qy      201 IleguHISGlnLysCysGlnAsnAlaTyProGlnAsnIleThrAspThrMetValCys 220
Db      610 ATTGAGCACACGAAAGTGTGAAGACGCTTACCCGGCAACATCACAGACCATGTGTGT 669
Qy      221 AlaSerValGlnGlnGlyGlyAspSerCysGlnGlnIleAspSerGlyGlyProLeuVal 240
Db      670 GCCACGTCGACGAAAGGGGGCAAGACTCTCTCCAGGGTACTCCGGGGGCTCTGTGTC 729
Qy      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlnAspProCysAlaIleThrArg 260
Db      730 TGTAAACAGTCTCTTCAAGGCAATTATCTCTGGGGCGAGATCCGTTGTCCGATCACCCGA 789
Qy      261 LysProGlyValTyThrIleValCysIleTyValAspTrpIleGlnIleThrMetLys 280
Db      790 AAGCTGTGTGTCTACACGAAAGCTGTGCAAAATATGTGACTGTGATCCAGAGACGATGAAG 849
Qy      281 AsnAsn 282
Db      850 AACCAAT 855

```

RESULT 12

US-10-140-926-505

; Sequence 505, Application US/10140926

; Publication No. US2003013435A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

```

/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C187
/ CURRENT APPLICATION NUMBER: US/10/140,926
/ PRIOR APPLICATION DATE: 2002-05-07
/ PRIOR APPLICATION removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 505
/ LENGTH: 1204
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ US-10-140-926-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 12

US-09-856-320A-2 (1-282) x US-10-140-926-505 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaIa 20
DB 10 ATGCAGAGGTGAGTGGGCTGGCGGACTGAGAGTCACTCGGCGAGAGCTTCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
DB 70 AAGGAACCTGGGGCCCGGCTCTCCCTCCAGCCATGAGATTTCAGATTAACTCG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGluCys 60
DB 130 CTTCCTCTGGCAACAGGGCTTTGAGGGGAGAGACCGAGATCATCAAGGGGTTCCGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLeuThrArgLeuLeuCysGly 80
DB 190 AAGCCTCACTCCAGCCTGGGAGGAGCCCTGTTGAGAAAGCGGGCTACTCTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGCCTCATGCGCCCGCAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlyGlnThrArgThr 120
DB 310 ATATGTTCACTGGGAGGAGCAACCTCCAGAAAGAGAGAGGGCTGTAGCAGACCCGGACA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACGTGAGTCTCTCCCAAGCCCGGCTTCAACAAAGGCTCCCAACAAAGCAACCCG 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 430 AATGACATCATGCTGTGTAAGATGGCATGGCCAGTTCATCATCCGTGGCTGTGCAGACC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
DB 490 CTCACCTCTCTCTCAAGCTGTGTCACTGTGACCAACAGCTGCTCATTTCCGGCTGGGCG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 550 AGCAGCTTCAGGCCCAAGTTAGCGCTGCTCAACACTTCGAGATGGCCCAACATCACCATC 609
QY 201 IleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220

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DB 610 ATTGAGCACCAGAGTGTGAGAAAGCGCTACCCCGGCAATCATCAGACCATGTGTGT 669
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
DB 670 GCCAGCGTGCAGAAAGGGGCAAGAGCTCTCCAGGGTGAATCCGGGGCCCTCTGTGC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB 730 TGTAACTGCTCTCTTCAAGCACTTATCTCTGGGCCAGAGATCCGTGTGCATCACCGCA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnIleThrMetLys 280
DB 790 AAGCCTGTGTGTACAGCAAGATGTGCAAAATATGTGACTGTGATTCAGAGACGATGAAG 849
QY 281 AsnAsn 282
DB 850 AACCAAT 855

RESULT 13
US-10-141-698-505
/ Sequence 505, Application US/10/141698
/ Publication No. US20030134357A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroli, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C206
/ CURRENT APPLICATION NUMBER: US/10/141,698
/ PRIOR APPLICATION DATE: 2002-05-08
/ PRIOR APPLICATION removed - See Palm or File Wrapper
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 505
/ LENGTH: 1204
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ US-10-141-698-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 12

US-09-856-320A-2 (1-282) x US-10-141-698-505 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaIa 20
DB 10 ATGCAGAGGTGAGTGGGCTGGCGGACTGAGAGTCACTCGGCGAGAGCTTCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
DB 70 AAGGAACCTGGGGCCCGGCTCTCCCTCCAGCCATGAGATTTCAGATTAACTCG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGluCys 60

```

Db 130 CTGCTCTGGCAAGAGGCTTGTAGGGGAGAGACCATCATCATCAGGCTTCAGATGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
Db 190 AAGCTCATCTCCAGCCCTGGAGGAGCCCTGTTGAGAAAGACCGGCTACTCTGTGGG 249
QY 81 AATThrLeuIleAlaProArgTrpLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db 250 GCGAGCTCATGCCCCCAGATGGCTCTCGACAGAGCCCACTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlnGlnHisAsnLeuGlnLysGlnGlnGlyCysGlnGlnThrArgThr 120
Db 310 AATAGTTCACTGGGCGAGACACACTCCGAAAGAGAGAGGCTGTGAGAGACCCGGACA 369
QY 121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db 370 GCGACTGAGTCTCTCCCGACCCCGGCTTCAACAACAGCTCCCAACAAGACACCGC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db 430 AATGACATCATGCTGGTGAAGATGGCATGCGCATCTCCATCATCCTGGGCTGTGGAGCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db 490 CTCACCTCTCTCTCAAGCTGTGTCACTGCTGCGACCAAGCTGCTCATTTCCGGCTGGGG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db 550 AGCAGCTTCAGCCCGACAGTTACGCTGCTGACACCTTCGATGCGCAACATCACCATC 609
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlnAsnIleThrAspThrMetAlaCys 220
Db 610 ATTGAGCACCAAGAGTGAAGACCGCTTACCCCGCAACATATACAGACCACTGATGTGT 669
QY 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlnLysAspSerGlyGlyProLeuVal 240
Db 670 GCCACGTCGCAAGAAAGGGGGCAAGGACTCTCTCCAGGGTGAATCCGGGGGCTCTGTGTC 729
QY 241 CysAsnGlnSerLeuGlnGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db 730 TGTAAACGAGTCTCTTCAAGGCAATTATCTCTGGGGCCAGAGTCCGTGTGCGATCACCGA 789
QY 261 LysProGlnValTyrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
Db 790 AAGCTGTGTCTACACGAAGTCTGCAATATGTGACTGATCCAGAGACGATGAAG 849
QY 281 AsnAsn 282
Db 850 AACAAAT 855
RESULT 14
US-10-141-702-505
; Sequence 505, Application US/10141702
; Publication No. US20030134358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C208
; CURRENT APPLICATION NUMBER: US/10/141,702
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO: 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-702-505
Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-09-856-320A-2 (1-282) x US-10-141-702-505 (1-1204)
QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAla 20
Db 10 ATGCAAGAGTTGAGTGGCTGCGGACTGGAAGTCATCGGCAAGGCTCTACAGCAGCC 69
QY 21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
Db 70 AAGAACTGGGGGCGGCTCTCCCGCCCTCCAGGCGCATGAGATTCGCACTTATCTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlnThrArgIleIleLysGlyPheGlnCys 60
Db 130 CTGCTCGGCAACAGGCTGTGTAGGGGAGAGACAGAGATCATCAAGGGGTGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysTrpArgLeuLeuCysGly 80
Db 190 AAGCTCATCTCCAGCCCTGCGAGGAGCCCTGTTCGAAAGACCGGCTACTCTGTGGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db 250 GCGAGCTTCAGCCCGACAGTTGCTCTCTGACACAGCCCACTCCCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlnGlnHisAsnLeuGlnLysGlnGlnGlyCysGlnGlnThrArgThr 120
Db 310 AATAGTTCACTGGGCGAGACACACTCCGAAAGAGAGGCTGTGAGAGACCCGGACA 369
QY 121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db 370 GCGACTGAGTCTCTCCCGACCCCGGCTTCAACAACAGCTCCCAACAAGACACCGC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db 430 AATGACATCATGCTGGTGAAGATGGCATGCGCATCTCCATCATCCTGGGCTGTGGAGCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db 490 CTCACCTCTCTCTCAAGCTGTGTCACTGCTGCGACCAAGCTGCTCATTTCCGGCTGGGG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db 550 AGCAGCTTCAGCCCGACAGTTACGCTGCTGCGACCAAGCTGCTCATTTCCGGCTGGGG 609
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlnAsnIleThrAspThrMetAlaCys 220
Db 610 ATTGAGCACCAAGAGTGAAGACCGCTTACCCCGCAACATATCAAGACACCATGTGTGT 669
QY 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlnLysAspSerGlyGlyProLeuVal 240
Db 670 GCGAGCTTCAGGAAAGGGGGCAAGGACTCTGCGAGGATGACTCCGGGGGCTCTGTGTC 729
QY 241 CysAsnGlnSerLeuGlnGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db 730 TGTAAACGAGTCTCTTCAAGGCAATTATCTCTGGGGCGAAGATCCGTGTGCGATCACCGA 789


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QY      261  LysProGlyValIYrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
DB      790  AAGCCTGCTGTCTACACGAAGCTCTCAATATATGTGACTGATCCAGAGAGATGAGG 849

QY      281  AsnAsn 282
DB      850  AACAAAT 855

RESULT 15
US-10-141-704-505
; Sequence 505, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33081C209
; CURRENT APPLICATION NUMBER: US/10/141,704
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-704-505

Alignment Scores:
Pred. No.: 5,19e-162          length: 1204
Score: 1523.00              Matches: 282
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00%         Indels: 0
DB: 12                      Gaps: 0

US-09-856-320A-2 (1-282) x US-10-141-704-505 (1-1204)

QY      1  MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
DB      10  ATGCAGAGGTTGAGTGCGCTGCGGAGCTGGAAGTCATCGGCGAGAGGTCTCACAGCAGCC 69

QY      21  LysGluProGlyValIAsrSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
DB      70  AAGGAACCTGGGGCCGCTCTCCCTCCCGCCAGGCGCATGAGATTCTGCAGTTAAATCCCTG 129

QY      41  LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleLysGlyPheGluCys 60
DB      130  CTTGCTCTGGCAACAGGGCTTTAGGGGAGAGACCAAGATCATCAAGGGGTTGAGGTGC 189

QY      61  LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuCysGly 80
DB      190  AAGCTCACTCCAGGCTGCGCAGGAGGCTGTTGAGAAAGACCGGGCTACTCTGTGGG 249

QY      81  AlaThrLeuIleAlaIAsrProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB      250  GCGAGCGCTATCGCCCGCCAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCGCTAC 309

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QY      101  IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120
DB      310  ATAGTTTACCTGGGGGAGACACAACCTCCAGAAAGAGAGAGGCTGTGTAGCAGACCCGGAGA 369

QY      121  AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB      370  GCCACTGAGTCTCTCCCGCCAGCCCGCTTCAACAAACAGCTCCCAACAAACACACCCG 429

QY      141  AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB      430  AATGACATCATCTGTGTGAAGATGCAATCGCAATCTCCATCATCACTGGGGCTGTGCAACCC 489

QY      161  LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
DB      490  CTCACCTCTCTCTACGCTGTCTACTGTGSCACCAAGCTGCTCATTTCCGGCTGGGGC 549

QY      181  SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB      550  AGCAGGTCCAGCCCGCCAGTTAGCCTGCTCACCCTTGCGATGCGCCAAATCACCATC 609

QY      201  IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
DB      610  ATTGAGCACCAAGATGTGAGAACCGCTTACCCCGCCAAACATCACAGACACCATGTGTGT 669

QY      221  AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
DB      670  GCCACGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 729

QY      241  CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB      730  TGTAAACCAAGTCTCTCAAGGCAATTATCTCTGCGGCGCAGAGATCCGTGTGCGATCACCCGA 789

QY      261  LysProGlyValIYrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
DB      790  AAGCTGCTGTCTACACGAAGCTCTCAATATATGTGACTGATCCAGAGAGATGAGG 849

QY      281  AsnAsn 282
DB      850  AACAAAT 855

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Search completed: October 23, 2003, 19:28:16
Job time : 322.593 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2003, 15:49:37 ; Search time 16.5558 Seconds
(without alignments)
1638.073 Million cell updates/sec

Title: US-09-856-320A-2

Perfect score: 1523

Sequence: 1 MGRRLRLRMKSSGRGLTAA.....GYTVCKYVDWIOETMKN 282

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	698.5	45.9	260	2	156559
2	618.5	40.6	261	2	A31136
3	617.5	40.5	265	1	KQRT
4	612	40.2	248	2	S55066
5	611.5	40.2	259	2	B31136
6	611.5	40.2	261	1	NGMSG
7	604.5	39.7	263	2	SI5686
8	602.5	39.6	246	1	TRRT2
9	601.5	39.5	261	2	A34079
10	600.5	39.4	246	1	TRRT1
11	596.5	39.2	261	2	A29586
12	595.5	39.1	259	1	KORTN
13	595	39.1	261	2	A29745
14	594	39.0	238	2	S31779
15	591.5	38.8	261	2	S45303
16	585.5	38.4	246	2	B25528
17	585	38.4	261	2	A25606
18	580.5	38.1	261	1	KOMS1
19	580	38.1	231	1	TRGTR
20	580	38.1	262	1	KQRT
21	578.5	38.0	244	2	A44284
22	578	38.0	232	1	KQPG
23	576	37.8	247	1	TRDG
24	572.5	37.6	257	2	S31772
25	571.5	37.5	263	2	S01971
26	569	37.4	229	1	A51968
27	569	37.4	229	1	TRBOTR
28	567	37.2	247	2	A27547
29	565	37.1	243	2	A35871

30	565	37.1	256	1	NGMSA	7S nerve growth fa
31	564.5	37.1	261	2	A41020	tissue kallikrein
32	564	37.0	259	2	A29746	tissue kallikrein
33	563	37.0	247	2	S13813	trypsin (EC 3.4.21
34	563	37.0	248	2	S55067	trypsin (EC 3.4.21
35	562.5	36.9	261	1	A32297	semenogelase (EC 3
36	559.5	36.7	261	1	S35711	semenogelase (EC 3
37	559	36.7	242	2	S49489	trypsin (EC 3.4.21
38	559	36.7	247	2	S05494	trypsin (EC 3.4.21
39	558.5	36.7	259	2	D23863	tissue kallikrein
40	558.5	36.7	261	1	TRMSMS	tissue kallikrein
41	558	36.6	261	2	A24378	tissue kallikrein
42	556	36.5	246	1	TRDGC	trypsin (EC 3.4.21
43	555.5	36.5	231	2	S31778	trypsin (EC 3.4.21
44	553	36.3	261	2	JB0236	tissue kallikrein
45	551.5	36.2	239	2	A27207	tissue kallikrein

ALIGNMENTS

RESULT 1

156559
neutropsin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: 156559
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishi, J. Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease ger
A:Reference number: 156559; MUID:95348817; PMID:7623137
A:Accession: 156559
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: GB:ID0785; NID:91648847; PIDN:BA06451.1; PID:G1020091
C:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRY>

Query Match 45.9%; Score 698.5; DB 2; Length 260;

Best Local Similarity 52.0%; Pred. No. 3.9e-54;

Matches 129; Conservative 35; Mismatches 77; Indels 7; Gaps 3;

QY	39	ILLALATGVGGER-----ITKECKRPHSQPQALPEKTRLLCGATLIAPRLTLTA	93
DB	13	ILLLEFMGAMAGLTAAQSKILEGRICPHSQPQALFQGERLLCGVLGDRWLTLTA	72
QY	94	HCLKPRYIVHGOHNLQKEEGCEOTRTATESPFPHPGPNNSLPNKDRNDIMLVKMASPVS	153
DB	73	HCKKQKIVRIGDHSLSRDPQDEIQVAQSIQHFCTYNSNP-EDHSHDILIRLQNSAN	131
QY	154	ITWAVRPLTLSSRCVTAGTSLISGMSGTSSPOLRPLTLRCANITIIHOKCENAYRPN	213
DB	132	LGDVKVPQLANLCPKVQOKCIISGCGTIVTSPOENFPTLNCABEVKISQNKCEAYGCK	191
QY	214	ITDITWVCAVSGEGDSCQSPSGPLVNCOSLOGIISGQPCATITRRKPGVTVTKCKYVD	273
DB	192	ITBGNVCAG-SSNGADTQDSGGLVCDGMLQGITSGSDPCGKPERKPGVTVTKICRYTT	250
QY	274	WIOETMKN 281	
DB	251	WIKTMDN 258	

RESULT 2

A31136
tissue kallikrein (EC 3.4.21.35) 7 precursor, submandibular - rat
N:Alternate names: glandular prokallikrein 7, submandibular; proteinase A
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 22-Jun-1999
C:Accession: A31136; S10698; S10699; D41429; B41429; S09315
R:Chen, Y.P.; Chao, J.; Chao, L.
Biochemistry 27, 7189-7196, 1988

A:Title: Molecular cloning and characterization of two rat renal kallikrein genes.
A:Reference number: A1136, MUID:89088074, PMID:284998
A:Accession: A1136
A:Molecule type: DNA
A:Residues: 1-261 <CHE>
R:Elmouhamed, A., Gurnan, N.; Billiard, M.; Gauthier, F.
FEBS Lett. 265, 137-140, 1990
A:Title: Substrate specificity of two kallikrein family gene products isolated from the
A:Reference number: S10698, MUID:90306305, PMID:2194829
A:Accession: S10698
A:Molecule type: protein
A:Residues: 25-36 <ELM>
A:Accession: S10699
A:Molecule type: protein
A:Residues: 112-139 <EL2>
R:Kato, H.; Nakamishi, E.; Enyoji, K.; Hayashi, I.; Oh-Ichi, S.; Iwanaga, S.
J. Biochem. 107, 1389-1404, 1987
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: with
A:Reference number: A41429, MUID:88198057, PMID:3482210
A:Accession: D41429
A:Molecule type: protein
A:Residues: 112-133 <KAT>
A:Accession: B41429
A:Molecule type: protein
A:Residues: 25-34, 'D', 36-45, 'S', 47-67, 'X', 69-75 <KA2>
R:Brady, J.M.; MacDonald, R.J.
Arch. Biochem. Biophys. 278, 342-349, 1990
A:Title: The expression of two kallikrein gene family members in the rat kidney.
A:Reference number: S09315, MUID:90225801, PMID:2183721
A:Accession: S09315
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 43-45, 'S', 47-114, 'A', 116-261 <BRA>
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-261/Product: tissue prokallikrein 7, submandibular #status predicted <MAR>
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

[illegible]

```
RESULT 3
KORP
tissue kallikrein (EC 3.4.21.35) precursor - rat
N;Alternate names: angiotensin kallikrein; kininogenin; true tissue kallikrein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 16-Jun-2000
A;Accession: A00944, A41429, A25137, JX0073, A23863, A33559
```

R.Swift, G.H.; Macgown, J.C.; Ashley, P.L.; Cummings, S.W.; Macdonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A>Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of t
A.Reference number: A00944; MUID:8j117659; PMID:6961406
A.Accession: A00944
A.Molecule type: mRNA
A.Residues: 1-265 <SWT>
A.Experimental source: pancreatic
R.Kato, H.; Nakanishi, E.; Enjoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A>Title: Characterization of serine proteinases isolated from rat submaxillary gland: with
A.Reference number: A41429; MUID:88j98057; PMID:3482210
A.Accession: A41429
A.Status: preliminary
A.Molecule type: protein
A.Residues: 29-53, 'X', '55-87 <KAT>
R.Gerald, W.L.; Chao, J.; Chao, L.
Biochim. Biophys. Acta 866, 1-14, 1986
A>Title: Immunological identification of rat tissue kallikrein cDNA and characterization
A.Reference number: A25137; MUID:86j31678; PMID:3004582
A.Accession: A25137
A.Molecule type: mRNA
A.Residues: 115-265 <GER>
R.Inoue, H.; Fukui, K.; Miyake, Y.
J. Biochem. 105, 834-840, 1989
A>Title: Identification and structure of the rat true tissue kallikrein gene expressed in
A.Reference number: JX0073; MUID:89j27211; PMID:2753879
A.Accession: JX0073
A.Molecule type: DNA
A.Residues: 1-265 <INO>
A.Cross-references: GB:D00448; NID:9220792; PIDN:BAA00346.1; PID:9220794
A.Experimental source: kidney
R.Ashley, P.L.; Macdonald, R.J.
Biochemistry 24, 4512-4520, 1985
A>Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
A.Reference number: A23863; MUID:86051477; PMID:2998455
A.Accession: A23863
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-265 <ASH>
A.Cross-references: GB:M11563; NID:9205029; PIDN:AAA1464.1; PID:9205030
A.Experimental source: submaxillary gland
R.Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; Macdonald, R.J.
J. Biol. Chem. 264, 7653-7662, 1989
A>Title: Organization and expression of the rat kallikrein gene family.
A.Reference number: A33359; MUID:89214217; PMID:2708383
A.Accession: A33359
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 5-265 <WIN>
A.Cross-references: GB:M23874; GB:J04701; GB:M23875; GB:M23876; NID:9205007; PIDN:AAA414
C.Comment: The kallikreins liberate lysyl-bradykinin, a vasactive decapeptide, from kin
C.Comment: The protein presumably assumes the two-chain form by cleavage between residue
C.Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release I
C.Genetics:
A.Introns: 73/2: 169/1; 214/3
C.Superfamily: trypsin; trypsin homology
C.Keywords: hydrolase; pancreas; serine proteinase; zymogen
F.I-17/Domains: signal sequence #status predicted <SIG>
F.I-18-28/Domains: activation peptide #status predicted <APT>
F.I-29-265/Product: tissue kallikrein, pancreatic #status predicted <MPR>
F.I-29-257/Domains: trypsin homology <TRY>
F.I-35-177, 54-70, 156-223, 188-202, 213-238/Disulfide bonds: #status predicted
F.I-69, 124, 217/Active site: His, Asp, Ser #status predicted

Query Match	40.5%	Score	617.5	DB	1	Length	265
Best Local Similarity	43.88%	Pred.	No	5,6e-47			
Matches	112	Conservative	48	Mismatches	85	Indels	11
				Gaps	2		

Qy	38	LILALATGLVG---	ETRIIKGFCKPHSQPQALAFKTRLLCGATLIAPRWLLTAA	93
bb	9	ILFLALISGRDAAFPVQSRVVGCGYNENMSQPMQAVVYFGEYLICGCVLLIDPMSWVITAA	68	

Oy 38 LILIALATGIVGC---ETRIIKGFEECKPHSQWQALAEFKTRLLOCATIADRWLLTAA 93
 :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Dd 9 ILFLALSLGRNDAAPVQSRVVGVCNCEMNSQWQAVVVYFGEYLTCGVVLIDPSWITAA 68

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OY      94 HCLKPRVIYHLOOHNLQKEGCEQOTTAATESPFHPENFNSL-----PKXDRANDIMLV 146
Db      69 HCATTNYQVLRNRLNIYEDPEPPQAHLVSOQSPFHPENODLIWNHTROQPEDDYNDIMLTL 128

OY      147 KMASPVSIITMAVRPLTILSSRCVTAGTSCILISGWGTSSTPOLRLPHTLRCAITIIISHOKC 206
Db      129 HLSQGADIDVGKVIDLPIEPRKVGSTCLASGWSGITTPGLEISDDLCQCNIDLLSNEKC 188

OY      207 ENAYRGNTITDYNVCAVSQEGKXDSCOGSDGGPLVNCQSLIGIISWQODPCALTRRKRGVYT 266
Db      189 VEAHKEEVLDTMLCAGEMGGKXDTCKSDGGPLICNGVILQGISWGFNPGCBPKKGIYT 248

OY      267 KVCCKYVDIMQETMKKN 282
Db      249 KLIKFTPMKEVWKEN 264

```

RESULT 4
S55066
trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N/Alternate names: trypsinogen II
C/Species: Gallus gallus (chicken)
C/Date: 23-Aug-1995 #sequence_revistion 19-Oct-1995 #text_change 22-Jun-1999
C/Accession: S55066; S72347
R/Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A/Title: Isolation and characterization of the chicken trypsinogen gene family
A/Reference number: S55065; MUID:9551611; PMID:7733885
A/Accession: S55066
A/Molecule type: mRNA
A/Residues: 1-248 <MAN1>
A/Cross-references: EMBL:U15157; NID:G603906; PIDN:AAAT9914.1; PID:G603907
A/Experimental source: clone 2-P29
A/Accession: S72347
A/Molecule type: DNA
A/Residues: 1-248 <MAN2>
A/Cross-references: EMBL:U15157; NID:G603906; PIDN:AAAT9914.1; PID:G603907
A/Experimental source: clone 2-P29
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F.1-16/Domain: signal sequence #status predicted <SIG>
F.17-25/Domain: activation peptide #status predicted <APT>
F.26-248/Product: trypsin II #status predicted <MAT>
F.26-241/Domain: trypsin homology <TRY>
F.65,109,202/Active site: His, Asp, Ser #status predicted

Query Match	40.2%	Score 612	DB 2:	Length 248
Best Local Similarity	48.2%	Pred No. 1.6e-46		
Matches	121	Conservative	38	Mismatches 82
			Indels 10	Gaps 5

QY	33	MRILDLI-L-LALATGLVGG-ETRIIKGFEECKPHSQPMQALFEXTRLLCATLIAPRW	88
Db	1	MKFLFLILISLGGAAAFPGAGDDDDIIVGGYTQPREHSPVQVBL-NSGYHFHCGGSLINSQW	59
QY	89	LITAAHCKLPRIYVHLGQHNILQKEGCEQTRTATESPFIHGGNSLSPNDRHNDMLVQM	148
Db	60	VLSAAHCKRSKIQVNLGGEINIVQDESEVYKSSVIYIRHFKSSITLN---NDIMLIRL	115
QY	149	ASPVSIITAAVRPLTILSSRCVTAGTISCLISGWSTSSPOLRLPHTLRCAINITIIIEHKQEN	208
Db	116	ASAAVEYSADIDPIALFPSSCAKAGTECLISGMWNTLSNGYNYBELQLCLAAPIILSDQECOE	175
QY	209	AYPGNITPTWCAASVOEGSGKDSQOEDSGPELVTCNQSLQIISWGDPCAITRKPGVYTRV	268
Db	176	AYPGDITSNMTLGVGLEGGKDSQOEDSGPVPVCCNELQGIIVSWGIG-CALKGYPGVYTRV	234
QY	269	CKYVDMIOETM	279
Db	235	CNYVDMIOETI	245

tissue kallikrein (EC 3.4.21.35) 3 precursor, submandibular - rat
M.Alternate names: glandular prokallikrein 3, submandibular
C.Species: Rattus norvegicus (Norway rat)
C.Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 22-Jun-1999
C.Accession: B31136
R.Chen, Y.P.; Chao, J.; Chao, L.
Biochemistry 27, 7189-7196, 1988
A.Title: Molecular cloning and characterization of two rat renal kallikrein genes.
A.Reference number: A31136; MVID:89088074; PMID:2849988
A.Accession: B31136
A.Molecule type: DNA
A.Residues: 1-259 <CHE>
A.Cross-references: GB:M19648; GB:J02837; NID:9205002; PIDN:AA51640.1; PID:g2050006
A.Note: the authors translated the codon GTC for residue 230 as Cys
C.Superfamily: trypsin; trypsin homology
C.Keywords: hydrolase; serine protease
F.1-18/Domain: signal sequence #status predicted <SIG>
F.19-259/Product: tissue prokallikrein 3, submandibular #status predicted <MAT>
F.63-251/Domain: trypsin homology <TRY>
F.63,118,211/Active site: His, Asp, Ser #status predicted

[illegible]

RESULT 6

NGMSG

7S nerve growth factor gamma chain (EC 3.4.21.-) precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Dec-1981 #sequence revision 17-May-1985 #text change 18-Jun-1999

C:Accession: A91005; A90949; A93510; A92341; A00942; A21093; A22705

R:Evans, B.A.; Richards, R.I.

EMBO J. 4, 133-138, 1985

A:Title: Genes for the alpha and gamma subunits of mouse nerve growth factor are contiguous

A:Reference number: A91005; MUID:85257431; PMID:3848339

A:Accession: A91005

A:Molecule type: DNA

A:Residues: 1-261 <EVA>

R:Ullrich, A.; Gray, A.; Wood, W.I.; Hayflick, J.; Seeburg, P.H.

DNA 3, 387-392, 1984

A:Title: Isolation of a cDNA clone coding for the gamma-subunit of mouse nerve growth factor

A:Reference number: A90949; MUID:85076169; PMID:6548955

A:Accession: A90949

A:Molecule type: mRNA

A:Residues: 1-261 <ULL>

A:Cross-references: GB:X01389; NID:G53373; PIDN:CAA2545.1; PID:G53374

R:Howles, P.N.; Dickins, D.P.; DiCaprio, L.L.; Woodworth-Gutai, M.; Gross, K.W.

Nucleic Acids Res. 12, 2791-2805, 1984

A:Title: Use of a cDNA recombinant for the gamma-subunit of mouse nerve growth factor to

A:Reference number: A93510; MUID:84169573; PMID:6200835

A:Accession: A93510

A:Molecule type: mRNA


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      115 SPVKLNARVATVALPSSCAPAGTQCLISGWNLTSSGVNPDLLQCLDAPLPLPOADCEAS 174
      210 YPGNITDPMVCAVVOEGKDSGCGSGPVLVNOISLOGIISWGQDPCAIRKRGVYTKVC 269
      175 YPKITIDNMVCGVFLBEGKDSGCGSGPVLVNOISLOGIISWGQDPCAIRKRGVYTKVC 233
      270 KYVDWIQETMKNN 282
      234 NYVDWIQDTIAAN 246

RESULT 9
A34079
tissue kallikrein (EC 3.4.21.35) P1 precursor - rat
N:Alternate names: kallikrein-related proteinase K8
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 22-Jun-1999
C/Accession: A34079; S10700
R:Brady, J.M.; Wines, D.R.; MacDonald, R.J.
Biochemistry 28, 5203-5210, 1989
A:Title: Expression of two kallikrein gene family members in the rat prostate.
A:Reference number: A34079; PMID:89352606; PMID:2765531
A:Accession: A34079
A:Status: preliminary
A:Molecule type: DNA; mRNA
A:Residues: 1-261 <BRA>
A:Cross-references: GB:M27215; GB:M27216; GB:M27217; NID:g206638; PIDN:AAA42036.1; PID:g
A:Experimental source: prostate
R:Blomj r, A.; Gutman, N.; Brillard, M.; Gauchier, F.
FEBS Lett. 265, 137-140, 1990
A:Title: Substrate specificity of two kallikrein family gene products isolated from the
A:Reference number: S10698; PMID:90306305; PMID:2194829
A:Accession: S10700
A:Molecule type: protein
A:Residues: 25-43;112-138 <ELM>
A:Experimental source: submaxillary gland
A>Note: 125-Lys was also found
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:25-253/Domain: trypsin homology <TRY>
F:25-111/Product: tissue kallikrein P1 light chain #status experimental <MAT1>
F:112-261/Product: tissue kallikrein P1 heavy chain #status experimental <MAT2>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 39.5%; Score 601.5; DB 2; Length 261;
Best Local Similarity 43.0%; Pred. No. 1.4e-45;
Matches 111; Conservative 46; Mismatches 90; Indels 11; Gaps 2;

      36 LQILALATNG---LVGETRIIKGECKPHSQPQWQALFEKTRLLCGATLIAPRWLT 91
      3 LILFILSLGWMDAAPQOSRIIGFNCBKNSQPVAVYHNEPQCGGLVHPSWLT 62
      92 AAHCLKRYIVLHGOHNLQKEGCEQTRTATESFPHPGFNNSTL-----PNKDRNDIM 144
      63 AAHCVSVNVQVWLGRNNLLEDEPFAGRLVSGSFHPHGNLDLIKHTKPKGNDYNDLM 122
      145 LYKMASPVSTIAVRLTSSRCVTAGTSCILISGKSTSPQRLPHTLRCANITTIHQ 204
      123 LHLKTPADITGVKVIDPTEPRKVGSTCLTSGWGSIPPLKWEFPDDLIQCVNIHLISNE 182
      205 KCEENVPGNITDPMVCAVVOEGKDSGCGSGPVLVNOISLOGIISWGQDPCAIRKRGV 264
      183 KIKIAYNDVTVMLCAGMDGDKICKDSSGGLICDGLVGLTISGWSMPCGEPNKPSEV 242
      265 YTRKCKRYVDWIQETMKNN 282
      243 YTKLIKFTSMKKVKMEN 260

RESULT 10
TRRTI
trypsin (EC 3.4.21.4) I precursor - rat

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N:Alternate names: trypsinogen I
C:Species: Rattus norvegicus (Norway rat)
C>Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 24-Sep-1999
C/Accession: B22657; A00948
R:Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A:Title: Structure of two related rat pancreatic trypsin genes.
A:Reference number: A22657; PMID:85054880; PMID:6094547
A:Accession: B22657
A:Molecule type: DNA
A:Residues: 1-246 <CRA>
A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
A>Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 1
R:MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
A:Title: Two similar but nonallelic rat pancreatic trypsin genes. Nucleotide sequences o
A:Reference number: A00948; PMID:82265624; PMID:6896710
A:Accession: A00948
A:Molecule type: mRNA
A:Residues: 1-246 <MAC>
A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
C/genetics:
A:introns: 14/1; 67/2; 152/1; 197/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APR>
F:24-246/Product: trypsin I #status predicted <ENZ>
F:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F:63,107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.4%; Score 600.5; DB 1; Length 246;
Best Local Similarity 46.6%; Pred. No. 1.6e-45;
Matches 118; Conservative 40; Mismatches 88; Indels 7; Gaps 4;

      30 LQAMRILOLILALATNGLVGGETRIIKGECKPHSQPQWQALFEKTRLLCGATLIAPRWLT 89
      1 MSALILALVGAAPVPL-EDDDKIVGGTTCHEHVPVQVSL-NSGYHFGSGLINDQVW 58
      90 LTAHCLKRYIVLHGOHNLQKEGCEQTRTATESFPHPGFNNSTL-----PNKDRNDIMLVKMA 149
      59 VSAHCYKSRIVRGENHINVLBEGDEQFINAKIKHPNYSWTLN-----NDIMLIKIS 114
      150 SPVSITMAVRLPTLSSRCVTAGTSCILISGKSTSPQRLPHTLRCANITTIHQKCEA 209
      115 SPVKLNARVAPALPSACAPACTQCLISGWNLTSSGVNPDLLQCLDAPVLSQADCEA 174
      210 YPGNITDPMVCAVVOEGKDSGCGSGPVLVNOISLOGIISWGQDPCAIRKRGVYTKVC 269
      175 YPKITIDNMVCGVFLBEGKDSGCGSGPVLVNOISLOGIISWGQDPCAIRKRGVYTKVC 233
      270 KYVDWIQETMKNN 282
      234 NYVDWIQDTIAAN 246

RESULT 11
A29586
tissue kallikrein (EC 3.4.21.35) hGK-1 precursor - human
N:Alternate names: glandular kallikrein
C:Species: Homo sapiens (man)
C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 22-Jun-1999
C/Accession: A29586
R:Schedlich, L.J.; Bennetts, B.H.; Morris, B.J.
DNA 6, 429-437, 1987
A:Title: Primary structure of a human glandular kallikrein gene.
A:Reference number: A29586; PMID:88054467; PMID:2824146
A:Accession: A29586
A:Molecule type: DNA
A:Residues: 1-261 <SCH>
A:Cross-references: GB:M8157; NID:g186640; PIDN:AAA74454.1; PID:g386842

```

A; Note: the authors translated the codon TAC for residue 43 as Trp
C; Genetics: 15/3 25/3 15/3 21/3

A: Introns: 16/1; 69/2; 165/1; 210/3
C: Superfamily: trypsin; trypsin homology
C: Keywords: hydrolase; serine proteinase
F: 25-253/Domain: trypsin homology <TRY>
F: 65, 120, 213/Active site: His, Asp, Ser

Query Match	39.2%;	Score 596.5;	DB 2;	Length 261;
Best Local Similarity	43.4%;	Pred. No. 3.9e-45;		
Matches 11;	Conservative 48;	Mismatches 86;	Indels 11;	Gaps 2

Qy	38	LILIALATGVLVG----	ERRIIKGFECRPHNSQPMOAALEFKRLLCGATLLAPRWLLTAA	93
	::	::	::	::
	::	::	::	::
Db	5	VLSIALSVGCTGAVPLIQSRIVGSGMECEKHSQPMQAVAYSHQMAHGCVLVHNPQVLTAA	64	
Qy	94	HCLKPRYIYHLGCHNOKEBEGCEQIRTATSEFPHGFNNLS-----PKQDHRNDIMLV	146	
	::	::	::	::
	::	::	::	::
Db	65	HCKKKSQVWLGNHNLFEPEDTGORVAVSHSEPHPLYNNSLLKHQSLLRPDEDSHSDMLL	124	
Qy	147	KMASPVSIITAVVRPLTLSSRCVYAGTSCLSIGMGSTSSPOLRPLPTLRCAIITIIIEHQK	206	
	::	::	::	::
	::	::	::	::
Db	125	RLEBPARKITDVVKVLGIPTOBPRLGTTCTYASGSGSIIEPEEFLRPSLSCVSLHLISDMC	18	
	::	::	::	::
	::	::	::	::
Qy	207	ENAYPGNIITDTWVCASVOEGSGSCGDSGGLVNCOSLOGIISWGODPCAITRKPGYTT	266	
	::	::	::	::
	::	::	::	::
Db	185	ARAYSEKVTBFLMCAGIMTGGKDTCCGDSGGPLVCGVLTGQITSGPEPCALPEKPAVYT	244	
Qy	267	KVCKYVDIMIOETMKNN	282	
	::	::	::	::
	::	::	::	::
Db	245	KVHVYRKWKIDTITAA	260	

RESULT 12
KORTN

tonin (EC 3.4.21.-) precursor - rat
 N.Alternate names: esterase 1
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 25-Feb-1985 #sequence_revision 02-Dec-1994 #next_change 18-Jun-1999
 C.Accession: B31355, A131340, C23853, A94635, A34050, A30971, A009944
 R.Wines, D.R.; Brady, J.M.; Fitzcarr, D.B.; Roberts, J.L.; MacDonald, R.J.
 J. Biol. Chem. 264, 7657-7662, 1989
 J.Title: Organization and expression of the rat kallikrein gene family.

A:Reference number: A33359; MUID:89214217; PMID:2708383
A:Accession: B33359
A:Molecule type: DNA
A:Residues: 1-259 <MIN>
A:Cross-references: GB:M23877; GB:J04702; GB:M23878; NID:g207411; PUDN:AAA2259.1; PUD:5
R:Shai, S.Y., Woodley-Miller, C.; Chao, J.; Chao, L.
Biochemistry 28, 5334-5343, 1989
A:Title: Characterization of genes encoding rat tonin and a kallikrein-like serine prote
A:Reference number: A32340; MUID:89375248; PMID:2550051

A:Accession: A32340
A:Molecule type: DNA
A:Residues: 1-259 <SHA>
A:Cross-references: GB:M26533, NID:g206775, PIN:AAAA2081.1, PID:g206776, GB:J028650

A:Ashley, P.L., Macdonald, R.J.
Biochemistry 24, 4512-4520, 1985
A:Title: Kallikrein-related MRNAs of the rat submaxillary gland: nucleotide sequences of
A:Reference number: A23863; MUID:86051477; PMID:2998455
A:Accession: C23863
A:Molecule type: mRNA
A:Residues: 1-259 <ASH>
A:Cross-references: GB:M1565; NID:g205033; PID:AAA41466.1; PID:g205034
A:Lezure, C., Leduc, R., Seidah, N.G., Thibault, G., Gensec, J., Chretien, M.

Nature 307, 555-558, 1984
A:Title: Amino acid sequence of rat submaxillary tonin reveals similarities to serine protease
A:Reference number: A93333; MUID:84117504; PMID:6320014
A:Accession: A93333
A:Molecule type: protein
A:Residues: 25-259 <PA1>
R:Lazure, C.
Submitted to the Protein Sequence Database, March 1985

A;Reference number: A94635
A;Contents: carbohydrate-binding site; revisions
A;Accession: A94635

A: Molecule type: Protein
A: Residues: 104-119 <AA2>
R: Kanada, M., Furuhata, N., Yamaguchi, T., Ikekita, M.: Kizuki, K., Moriya, H. Biochem. Biophys. Res. Commun. 166, 231-237, 1990
A: Title: Observation of tissue prokallikrein activation by some serine proteases, arginyl
A: Reference number: A34050; MUID: 90147705; PMID: 2302205

A/Accession: A34050
A/Molecule type: protein
A/Residues: 25-30, 'X', 32-34 <KAM>
R/Liaure, C.; Leduc, R.; Seidau, N.G.; Thibault, G.; Genest, J.; Chretien, M.
Biochem. Cell Biol. 65, 321-337, 1987
A/Title: The complete amino acid sequence of rat submaxillary gland tonin does contain
;Reference number: A30971; MUID: 8721223; PMID:308148

A:Accession: A30971
A:Molecule type: protein
A:Residues: 25-259 <LAZ>
C:Comment: This protein is found in submaxillary gland. It has both trypsin- and chymotrypsin-like activities.
C:Genetics:
A:Introns: 16/1; 67/2; 163/1; 208/3

C:Superfamily trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; serine proteinase
F:1-17/Domain: signal sequence #stratus predicted <SIG>
F:18-24/Domain: propeptide #status predicted <PRO>
F:25-259/Product: tonin #stratus experimental <MAT>
F:25-251/Domain: trypsin homology <TRY>

Query Match	39.1%	Score 595.5;	DB.1	Length 259;
Best Local Similarity	42.2%	Pred. NO. 4.7e-45;		
Matches 109;	Conservative 51;	Mismatches 85;	Indels 13;	Gaps 3

QY 36 LQILALATGLVG---GETRIINGEPCEKHSOPMOAAFEKTRLLCGATLLAPRMLL 91

Db 3 LQTLSTLVLSVGRIDAPPGOSRIIVGGYCKENSGPMQVAVINE--YLGGCVLLIDPSVIT 60

QY 92 AAACLTPRITVHGGHNLQKEGCEQOTATATESPPHGF-----NNSLPNKHRRDIM 144

Db 61 AATCYNNYQVLLGRNNLFKDEPRFQRLVQSRHRHDYIPLYINTDDEGVNHDNDLM 120

QY 145 LVKMASPVSIWAVRPLTTSRCAVTAGTSCILSCMGSTSSPOLRLPHTLRCAIITIIIEHQ 204

Db 121 LHLSPRAPIITGVGVYIDLPTKEPVKSTCLASMGSTINSEMVASIDLCVAVIHLSNE 180

QY 205 KCENAPGNIITPMVCAISOEGKXSCGSDSGCLVYNOSLQGIISMGDPCCAIITRKPGV 264

Db 181 KCIETYKDNVTDVMLCAGMEGGRKDTCAAGDGGPLLCDGLVQIGTSGATPCAKPKTPAI 240

QY 265 YTKVCKYVDVIOETMKN 282

Db 241 YAKLIKFISWIKKVEN 258

RESULT 13
A29745
tissue kallikrein (EC 3.4.21.35) MGK-9 precursor, submandibular - mouse
N:Alternate names: glandular kallikrein MGK-9; major epidermal growth factor-binding protein
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #ext_change 22-Jun-1999
C:Accession: C29746; A29745; A27120; I70015
R:Drinkwater, C.C.; Evans, B.A.; Richards, R.I.
Biochemistry 26, 6750-6756, 1987
A:Title: Mouse glandular kallikrein genes: identification and characterization of the gene
A:Reference number: A90522; MUID:88107594; PMID:3322387
A:Accession: C29746
A:Molecule type: DNA
A:Residues: 17261 <DBI>
A:Cross-references: GB:M17985; NID:g193476; PIDN:AAA37681.1; PID:g387166
A:Experimental source: strain BALB/c, salivary gland

R. Blaber, M.; Isaacson, P.J.; Bradshaw, R.A.
 Biochemistry 26, 6742-6749, 1987
 A:Title: A complete cDNA sequence for the major epidermal growth factor binding protein
 A:Reference number: A29745; MUID:88107593; PMID:3322386
 A:Accession: A29745
 A:Molecule type: mRNA
 A:Residues: 1-261 <BLA>
 A:Cross-references: GB:M17962; NID:9192997; PIDN:AAA37541.1; PID:9309212
 R:Isaacson, P.J.; Silverman, R.E.; Blaber, M.; Server, A.C.; Nichols, R.A.; Shooter, E.M.
 Biochemistry 26, 2082-2085, 1987
 A:Title: Epidermal growth factor binding protein: identification of a different protein.
 A:Reference number: A27120; MUID:87299636; PMID:3304419
 A:Accession: A27120
 A:Molecule type: protein
 A:Residues: 25-54;112-124, 'X',126-130;165-184, 'X',186-187, 'X',189-192 <ISA>
 R:Evans, B.A.; Drinkwater, C.C.; Richards, R.I.
 J. Biol. Chem. 262, 8027-8034, 1987
 A:Title: Mouse glandular kallikrein genes: Structure and partial sequence analysis of th
 A:Reference number: 155260; MUID:87250386; PMID:3036794
 A:Accession: 170015
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 70-122 <RES>
 A:Cross-references: GB:M16608; NID:9198500; PIDN:AAA39351.1; PID:9198506
 C:Comment: This sequence is one of approximately twenty-five members of a gene family on
 C:Genetics: KAL
 A:Gene: KAL
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase; zymogen
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-261/Product: tissue kallikrein MGK-9, submandibular #status experimental <MAT>
 F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 39.1%; Score 595; DB 2; Length 261;
 Best Local Similarity 42.1%; Pred. No. 5,3e-45;
 Matches 110; Conservative 53; Mismatches 86; Indels 12; Gaps 3;

QY 33 MIIILILALATGLVG---ETRIKFECKPHSQPQALFEKTRLLCGATLIAPRW 88
 DB 1 MFPLILFLFALSLGGIDAAPRVHSGFCKEKSQPHNVAVRYNEYICGVLIDANW 59
 QY 89 LITAAHCKPRYIVHLGOHNLQKEGCEQTRTATESFPHPGNNSL-----PKKDRHN 141
 DB 60 VITAAHCYBENKVSGLKNNLIEBESAOHRLVSSFLHPGYNRSJLHNNHHPEDYSN 119
 QY 142 DIMLVKMASPVASITVAVRPLTSSRCVTAAGTSCILISGWSSTSSPOLRLPHTLRCAITII 201
 DB 120 DMLRLSKPADITDVVKRIALPTEPRKLGSTCLASGWSSTTPFRQNAKDLQCVNLKL 179
 QY 202 ENQKENVATPGNITPTMVAASVOEGKDSQCGDSGPLVNCNLSGIIISWGDDPCAIRTK 261
 DB 180 PNEDEGKAHIEKVTDMVLCAGETDGGKDTCKDSSGGLICDGLVIGITSWGFPCGEPK 239
 QY 262 PGVYTKVCYVDMIOETMKN 282
 DB 240 PGVYTKLIKFTSWIKDTMAKN 260

RESULT 14
 S31779
 trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)
 C:Species: Salmo salar (Atlantic salmon)
 C:Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
 C:Accession: S66657; S31779
 R:Male, R.; Lorens, J.B.; Smalas, A.O.; Torrisen, K.R.
 Eur. J. Biochem. 232, 677-685, 1995
 A:Title: Molecular cloning and characterization of anionic and cationic variants of try
 A:Reference number: S66657; MUID:96035908; PMID:7556223
 A:Accession: S66657
 A:Molecule type: mRNA
 A:Residues: 1-238 <MAL>

A:Cross-references: EMBL:X70074; NID:964387; PIDN:CAA9679.1; PID:964388
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>
 F:8-15/Domain: activation peptide #status predicted <APR>
 F:16-238/Product: trypsin III #status predicted <MAT>
 F:16-231/Domain: trypsin homology <TRY>
 F:22-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted
 F:55,99,192/Active site: His, Asp, Ser #status predicted

Query Match 39.0%; Score 594; DB 2; Length 238;
 Best Local Similarity 46.3%; Pred. No. 5,8e-45;
 Matches 112; Conservative 39; Mismatches 85; Indels 6; Gaps 4;

QY 41 LALALGVGERIRIKFECKPHSQPQALFEKTRLLCGATLIAPRWLTAAHCKPRY 100
 DB 3 VAFAPRIDDEDKIVGVECKRNSASYOASL-QSGYHFCGGSLSTWVAASHCKRSR 61
 QY 101 IVHLGOHNLQKEGCEQTRTATESFPHPGNNSLPNKDRNDIMLVKMASPVASITVAVRP 160
 DB 62 QVRLGEHNIIVNVEGTEQRTDSKVIMHPSYNSR--NLD--NDIMLIKSKSPASLSYST 117
 QY 161 LTLSRCVTAAGTSCILISGWSSTSSPOLRLPHTLRCAITIIHQKCNAYPGNITDTWVC 220
 DB 118 VALPSSCASSGTRCLVSGWNLSSSNVPTLRCLDPIILSSSCNSAYPQOITSNMF 177
 QY 221 ASVOEGKDSQCGDSGPLVNCNLSGIIISWGDDPCAITRKRGVYTKYVDWIOETMK 280
 DB 178 AGFMGKGKDSQCGDSGPLVNCNLSGIIISWGDDPCAITRKRGVYTKYVDWIOETMK 236
 QY 281 NN 282
 DB 237 SN 238

RESULT 15
 S45303
 tissue kallikrein (EC 3.4.21.35) precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 20-Oct-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
 C:Accession: S45303; S38487
 R:Gauthier, E.R.; Dumas, C.; Chappdelain, P.; Tremblay, R.R.; Dube, J.Y.
 Biochim. Biophys. Acta 1218, 102-104, 1994
 A:Title: Characterization of canine pancreas kallikrein cDNA.
 A:Reference number: S45303; MUID:94250683; PMID:8193155
 A:Accession: S45303
 A:Molecule type: mRNA
 A:Residues: 1-261 <GAU>
 A:Cross-references: EMBL:X75479; NID:9414018; PIDN:CAA53210.1; PID:9414019
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-261/Product: tissue kallikrein #status predicted <MAT>
 F:25-253/Domain: trypsin homology <TRY>
 F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 38.8%; Score 591.5; DB 2; Length 261;
 Best Local Similarity 43.6%; Pred. No. 1.1e-44;
 Matches 112; Conservative 46; Mismatches 86; Indels 13; Gaps 2;

QY 39 ILLALATGLVG---ETRIKFECKPHSQPQALFEKTRLLCGATLIAPRWLTAA 92
 DB 4 LVLCLASLAGTGAAPVQSRILIGMDTKNSQPMQALHYSKFGCGGLVNHPEWVTA 63
 QY 93 AHCLKPRYIVHLGOHNLQKEGCEQTRTATESFPHPGNNSL-----LPNKDRNDIML 145
 DB 64 AHCINDNQWLGVYVNFHEHDTAQPVQVRSFPHENSLLLKKNHTLPREDVSHDML 123
 QY 146 VKMASPVASITVAVRPLTSSRCVTAAGTSCILISGWSSTSSPOLRLPHTLRCAITIIHQK 205
 DB 124 LRLAEPQAITDAVAVLPLTQEPQVSGTCVASGSIIEPDKFIYPDDIQLQCVDELLSNDI 183
 QY 206 CENAYPGNITDTWVCASVOEGKDSQCGDSGPLVNCNLSGIIISWGDDPCAITRKRGVY 265

Db	184	CANAHSQKVTBFLCAGHLEGGKDTCTVBDGGPLICDGVLOGITSMGHVPCGSPNMPAVY	243
Oy	266	TKVCKYVDNIQETMKN	282
Db	244	TKVISHLEWIKETMTAN	260

Search completed: October 22, 2003, 15:53:45
Job time : 17.5558 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 15:48:12 ; Search time 9.9346 Seconds

(without alignments)
1335.036 Million cell updates/sec

Title: US-09-856-320A-2

Perfect score: 1523

Sequence: 1 MORLFWLRDMKSSGRGLTAA.....GYTVKVCYKVDWIQETMKNN 282

Scoring table: BLOSUM62

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1355	89.0	250	1	KLKB_HUMAN
2	756	49.6	250	1	KLKB_HUMAN
3	701.5	46.1	260	1	NRPN_RAT
4	698.5	45.9	260	1	NRPN_MOUSE
5	692.5	45.5	256	1	KLKB_HUMAN
6	690	45.3	260	1	KLKB_HUMAN
7	687.5	45.1	277	1	KLKB_HUMAN
8	650.5	42.7	293	1	KLKB_HUMAN
9	632.5	41.5	251	1	KLKB_HUMAN
10	618.5	40.6	248	1	KLKB_HUMAN
11	618.5	40.6	261	1	KLKB_HUMAN
12	617.5	40.5	261	1	KLKB_HUMAN
13	612	40.2	248	1	KLKB_HUMAN
14	611.5	40.2	259	1	KLKB_HUMAN
15	611.5	40.2	261	1	KLKB_HUMAN
16	604.5	39.7	263	1	KLKB_HUMAN
17	602.5	39.6	246	1	KLKB_HUMAN
18	601.5	39.5	261	1	KLKB_HUMAN
19	600.5	39.4	246	1	KLKB_HUMAN
20	596.5	39.2	261	1	KLKB_HUMAN
21	595.5	39.1	259	1	KLKB_HUMAN
22	595	39.1	261	1	KLKB_HUMAN
23	594	39.0	238	1	KLKB_HUMAN
24	594	39.0	244	1	KLKB_HUMAN
25	586	38.5	246	1	KLKB_HUMAN
26	585.5	38.4	261	1	KLKB_HUMAN
27	580.5	38.1	261	1	KLKB_HUMAN
28	580	38.1	231	1	KLKB_HUMAN
29	580	38.1	262	1	KLKB_HUMAN
30	578.5	38.0	244	1	KLKB_HUMAN
31	578.5	38.0	246	1	KLKB_HUMAN
32	576	37.8	247	1	KLKB_HUMAN
33	572.5	37.6	243	1	KLKB_HUMAN

34	572.5	37.6	257	1	KLKB_HUMAN	007276 macaca fasc
35	572.5	37.6	261	1	KLKB_HUMAN	P15946 mus musculus
36	571.5	37.5	253	1	KLKB_HUMAN	P49862 homo sapien
37	569	37.4	244	1	TRV2_XENLA	P70059 xenopus lae
38	567	37.2	247	1	TRV3_RAT	P08426 rattus norv
39	567	37.2	258	1	KLKB_PAPHA	Q28773 papio hamad
40	565	37.1	243	1	TRV1_XENLA	P19799 xenopus lae
41	565	37.1	256	1	KLKB_MOUSE	P00757 mus musculus
42	564.5	37.1	261	1	KLKB_MOUSE	P36368 mus musculus
43	564	37.0	248	1	TRV1_CHICK	Q90627 gallus gall
44	564	37.0	259	1	KLKB_MOUSE	P15948 mus musculus
45	563	37.0	247	1	TRV2_BOVIN	Q29463 bos taurus

ALIGNMENTS

RESULT 1	ID	KLKB_HUMAN	STANDARD	PRT	250 AA.
AC	Q9UX77	O75837	Q9NS65		
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Kallikrein 11 precursor (EC 3.4.21.-) (Hippocastin) (Trypsin-like protease).				
GN	KLKB_HUMAN				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Hippocampus;				
RX	MEDLINE=98438738; PubMed=9765601;				
RA	Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;				
RT	"CDNA cloning and expression of a novel serine protease, TlSP.,"				
RL	Biochim. Biophys. Acta 1399:225-228(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RC	TISSUE=Hippocampus, and prostate;				
RX	MEDLINE=20329229; PubMed=10872828;				
RA	Mitsui S., Yamada T., Okui A., Komitani K., Uemura H., Yamaguchi N.;				
RT	"A novel isoform of a kallikrein-like protease, TlSP/PRSS20, is expressed in the human brain and prostate.,"				
RL	Biochem. Biophys. Res. Commun. 272:205-211(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	MEDLINE=20130117; PubMed=10662548;				
RA	Yousef G.M., Scottias A., Diamandis E.P.;				
RT	"Genomic organization, mapping, tissue expression, and hormonal regulation of trypsin-like serine protease (TlSP PRSS20), a new member of the human kallikrein gene family.,"				
RL	Genomics 63:88-96(2000).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=20510030; PubMed=11054574;				
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.;				
RT	"Moss P., Paepir B., Wang K.,"				
RL	"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.,"				
RL	Gene 257:119-130(2000).				
RN	[5]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	Lamerding J.E., McCreedy P.M., Skowronski E., Viswanathan V.;				
RA	Burhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.;				
RT	Pan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.;				
RL	Dandann L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.;				
RA	Andrieu T., Trankheim M., Attix C., Amico-Keller G., Coefield J.;				
RT	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.;				
RA	Arellano A., Sanders C., Ow D., Nolan M., Tong S., Kobayashi A.;				
RL	Olsen A.S., Carrano A.V.;				
RT	"Sequence analysis of chromosome 19q13.4.,"				

RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
 RN [6] SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=Testis;
 RC MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mollighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 CC -1- FUNCTION: POSSIBLE MULTIFUNCTIONAL PROTEASE. EFFICIENTLY CLEAVES
 BZ-PHE-ARG-4-METHYLCOMARYL-7-AMIDE, A KALLIKREIN SUBSTRATE, AND
 WEALY CLEAVES OTHER SUBSTRATES FOR KALLIKREIN AND TRYPSIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC IsoId=Q9UBX7-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9UBX7-2; Sequence=VSP_005402;
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKIN AND PROSTATE. ISOFORM
 1 IS EXPRESSED PREFERENTIALLY IN BRAIN; ISOFORM 2 IN PROSTATE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB012917; BAA33404.1; ALT_INT.
 DR EMBL; AB013730; BAA88713.1; -
 DR EMBL; AB041036; BAA96797.1; -
 DR EMBL; AF164623; AAD47815.1; -
 DR EMBL; AF243527; AAG33364.1; -
 DR EMBL; AC011473; AAG23257.1; -
 DR EMBL; BC022068; AAH22068.1; -
 DR HSSP; P00753; IDPO.
 DR MEROPS; S01.257; -
 DR Genew; HGNC:6359; KLK11.
 DR MIM; 604434; -
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser protease_Try.
 DR Pfam; PF00089; trypsin; 1
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen;
 KW Alternative splicing.
 FT SIGNAL 1 18
 FT PROPEP 19 21 POTENTIAL.
 FT CHAIN 22 250 ACTIVATION PEPTIDE (POTENTIAL).
 FT ACT_SITE 62 62 KALLIKREIN 11.
 FT ACT_SITE 110 110 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 110 110 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT ACT_SITE 203 203 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 28 163 BY SIMILARITY.
 FT DISULFID 47 63 BY SIMILARITY.
 FT DISULFID 135 237 BY SIMILARITY.
 FT DISULFID 142 209 BY SIMILARITY.
 FT DISULFID 174 188 BY SIMILARITY.
 FT DISULFID 199 224 BY SIMILARITY.
 FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 1 M -> MORLRRLRDKSSGRLTAKEGARSPLQAM
 (in isoform 2)
 FT SQ SEQUENCE 250 AA; 27466 MW; 192D910BBCDC7A56 CRC64;
 /FTId=VSP_005402.
 Query Match 89.0%; Score 1355; DB 1; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2,4e-116;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 MRIQLILALATGLVGGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPRWLLTA 92
 DB 1 MRIQLILALATGLVGGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPRWLLTA 60
 QY 93 AHCLKPRITVHLGQHNLOKEGCEQOTRATSPFHPGNNLSLPKDRNDIMLYKMASPV 152
 DB 61 AHCLKPRITVHLGQHNLOKEGCEQOTRATSPFHPGNNLSLPKDRNDIMLYKMASPV 120
 QY 153 SITMAVRPLTSSRCVTAETAGTSCILISGWSSTSSPOLRLPHTRCANITIEHQKCNAYPG 212
 DB 121 SITMAVRPLTSSRCVTAETAGTSCILISGWSSTSSPOLRLPHTRCANITIEHQKCNAYPG 180
 QY 213 NITDTMVCASVOEGSKDSCGDSGPLYCNOSLOGIISWGDPCALITRKPCVYTKCKYV 272
 DB 181 NITDTMVCASVOEGSKDSCGDSGPLYCNOSLOGIISWGDPCALITRKPCVYTKCKYV 240
 QY 273 DWIOETMKN 282
 DB 241 DWIOETMKN 250
 RESULT 2
 KLK9 HUMAN STANDARD; PRT; 250 AA.
 ID KLK9 HUMAN
 AC Q9UKQ9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-
 L3).
 GN KLK9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20118156; PubMed=10652563;
 RX Yousef G.M., Luo L.-Y., Diamandis E.P.;
 RT "Identification of novel human kallikrein-like genes on chromosome
 19q13.3-q13.4";
 RL Anticancer Res. 19:2843-2852(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20247258; PubMed=10783266;
 RX Yousef G.M., Diamandis E.P.;
 RT "The expanded human kallikrein gene family: locus characterization and
 molecular cloning of a new member, KLK-L3";
 RL Genomics 65:184-194(2000).
 RN (3)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20510030; PubMed=11054574;
 RX Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,

RA Moss P., Paepker B., Wang K.,
 RT "Sequencing and expression analysis of the serine protease gene
 cluster located in chromosome 19q13 region."
 RL Gene 257:119-130 (2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Lameudin J.E., McCready P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.,
 RA Dangnan L., Ertler A., Christensen M., Georgescu A., Ayala J., Liu S.,
 RA Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Diarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Atellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carraro A.V.,
 RT "Sequence analysis of chromosome 19q13.4";
 RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- TISSUE SPECIFICITY: SKIN, THYMUS, TRACHEA, CEREBELLUM AND SPINAL
 CC CORD.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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 CC -----
 DR EMBL: AF135026; AAD26427.2; -;
 DR EMBL: AF243527; AAG33362.1; -;
 DR EMBL: AC011473; AAG23255.1; -;
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.307; -;
 DR Genew: HGNC:6370; KLK9.
 DR MIM: 605504; -;
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser-protease_Try.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydroxylase; Serine protease; Glycoprotein; Signal.
 KM Hydroxylase; Serine protease; Glycoprotein; Signal.
 FT SIGNAL 1 15
 FT CHAIN 16 250
 FT ACT_SITE 63 63 KALLIKREIN 9.
 FT ACT_SITE 111 111 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 29 164
 FT DISULFID 48 64
 FT DISULFID 136 238
 FT DISULFID 143 210
 FT DISULFID 175 189
 FT DISULFID 200 225
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 250 AA; 27512 MW; F2785245B063E98B CRC64;
 Query Match 49 6%; Score 756; DB 1; Length 250;
 Best Local Similarity 57.0%; Pred. No. 9.7e-62;
 Matches 138; Conservative 37; Mismatches 67; Indels 0; Gaps 0;

DB 69 LWRLGHEHLIMKWECPQLFRVTFPPHGFNKLSDANDNDIMLRLPRQARLSPAVO 128
 QY 160 PLTSSRCVYTAGSCISISMGSTSSPOLPLPHTLRANTTIEHCKEENAYPENITDVM 219
 DB 129 PLNLSQTCVSPGQCICISGVAVSPKALFPVTLQCANSTILENKLCHNAYPGHISDML 188
 QY 220 CASVQCGKDSGCGSGGFLVNCOSLQGIISMGDCAITRRKGVYTKYKVDYDIQETM 279
 DB 189 CAGLWGGGSGSCGDSGGLVNCGLTAGVSGAEGFCSPRRPRAVYTSCHYIDMIQETM 248
 QY 280 KN 281
 DB 249 EN 250
 RESULT 3
 NRPN RAT STANDARD; PRT; 260 AA.
 ID NRPN RAT
 AC 088780;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neutropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
 DE protease 1).
 GN KLK8 OR PRSS19 OR NRPN OR BSP1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=Fischer; TISSUE=Brain;
 RX MEDLINE=98389725; PubMed=9722524;
 RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Latche R.;
 RT "Serine proteases in rodent hippocampus";
 RL J. Biol. Chem. 273:23004-23011 (1998).
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
 CC HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
 CC FIBRONECTIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO HIPPOCAMPUS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AJ005641; CA06643.1; -;
 DR HSSP: O61955; INPM.
 DR MEROPS: S01.244; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser-protease_Try.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydroxylase; Serine protease; Glycoprotein; Zymogen; Signal.
 KM Hydroxylase; Serine protease; Glycoprotein; Zymogen; Signal.
 FT SIGNAL 1 38
 FT PROPEP 29 32
 FT CHAIN 33 260
 FT ACT_SITE 73 73 NEUROPSIN.
 FT ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 39 173
 FT DISULFID 58 74
 FT DISULFID 145 246
 FT DISULFID 145 246 BY SIMILARITY.

Query Match 46.1%; Score 701.5; DB 1; Length 260;
 Best Local Similarity 52.4%; Pred. No. 9, 4e-57;
 Matches 129; Conservative 35; Mismatches 75; Indels 7; Gaps 3;

FT DISULFID 152 218 BY SIMILARITY.
 FT DISULFID 184 198 BY SIMILARITY.
 FT DISULFID 208 233 BY SIMILARITY.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 260 AA; 28510 MW; 58DF4F0602A087F5 CRC64;

39 ILLALATGIVGETR-----IIKGECKEPHSQPMQALFEKTRLLCGATLIPMLTAA 93
 13 ILLFLMGMAQLTTRAGSKIIIEGCECKHSQPMQALFGSRIVCGVLVDNRVLTAA 72
 94 HCLKPRYIVHIGQNLQKEEGCEQRTATSPHPGPFNNLSPNKDRNDIMLVKASPV5 153
 73 HKKKQKYSVRLGDHSIQKREDEPEQIOWARSIQHPFNSSNP-EDHSHDMLRLQNSAN 131
 154 IIMVAPRLTSSRCVTAGTSCISGWSSTSSPOLRLPHLRCAANTITIEHCKENAYRPN 213
 132 IGDKVKPIELANLCPKVGQKCTISGWTSTSPQENFPNTLCAEVKYSQNCERAYPEK 191
 214 IEDTWCASVQGGKSCQGGSGPLVNCQSLQGIISWGDDCATRKPGVYTKYCKYVD 273
 192 IIEGVACAG-SSNGADTCCGDSGGLVNCVGLQGITWGSDFCGKREKGVYTKICRTYN 250
 274 WIOETM 279
 251 WIKTMT 256

RESULT 4
 NRPN MOUSE
 ID NRPN MOUSE STANDARD; PRT; 260 AA.
 AC Q61955;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neutropin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).
 GN KLK8 OR PRSS19 OR NRPN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Hippocampus;
 RX MEDLINE=95348817; PubMed=7623137;
 RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
 Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
 "Expression and activity-dependent changes of a novel limbic-serine
 RT protease gene in the hippocampus."
 RT J. Neurosci. 15:5088-5097(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
 "Cloning and assignment of mouse neutropin gene, Prss19 to chromosome
 RT 7B4."
 RT Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
 RN (3)
 RP SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=98225202; PubMed=9556608;
 RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
 Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
 "Characterization of recombinant and brain neutropin, a
 RT plasticity-related serine protease";
 RT J. Biol. Chem. 273:11189-11196(1998).
 RN (4)
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
 RC TISSUE=Hippocampus;
 RX MEDLINE=99134351; PubMed=9933620;
 RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,

RA Shiosaka S., Hakoshima T.;
 RT "Crystal structure of neutropin, a hippocampal protease involved in
 RT kindling epileptogenesis."
 RL J. Biol. Chem. 274:4220-4224(1999).
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
 CC HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
 CC FIBROBLASTIN.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -1- ENZYME REGULATION: STRONGLY INHIBITED BY DIISOPROPYL
 CC FLUOROPHOSPHATE, LEUPEPTIN AND (4-AMIDINOPHENYL)METHANESULFONYL 1-
 CC FLUORIDE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE LIMBIC SYSTEM OF
 CC MOUSE BRAIN AND IS LOCALIZED AT HIGHEST CONCENTRATION IN PYRAMIDAL
 CC NEURONS OF THE HIPPOCAMPAL CA1-3 SUBFIELDS.
 CC -1- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260.
 CC -1- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: D30785; BAA06451.1; -.
 CC EMBL: AB032202; BAA92435.1; -.
 CC PIR: I56559; I56559
 CC PDB: INPM; 23-MAR-99.
 CC MEROPS: S01.244; -.
 CC MGD: MGI:992018; KLK8.
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR001254; Ser protease_Try.
 CC Pfam: PF00089; Trypsin_1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC SMART: SM00020; TRYPSIN_1.
 CC PROSITE: PS50240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC K01 Hydroxylase; Serine protease; Glycoprotein; Zymogen; Signal;
 CC 3D-structure.
 CC SIGNAL 1 28
 CC PROPEP 29 32
 CC ACT_SITE 33 260
 CC ACT_SITE 73 73
 CC ACT_SITE 120 120
 CC ACT_SITE 212 212
 CC DISULFID 39 173
 CC DISULFID 58 74
 CC DISULFID 145 246
 CC DISULFID 152 218
 CC DISULFID 184 198
 CC DISULFID 208 233
 CC CARBOHYD 110 110
 CC STRAND 34 34
 CC STRAND 37 38
 CC STRAND 41 42
 CC TURN 43 46
 CC TURN 47 52
 CC TURN 53 54
 CC TURN 55 64
 CC TURN 65 66
 CC STRAND 67 70
 CC STRAND 72 74
 CC HELIX 77 80
 CC STRAND 80 83
 CC STRAND 87 87
 CC TURN 88 89
 CC STRAND 96 98
 CC STRAND 100 105
 CC TURN 107 108
 CC TURN 114 115

N-LINKED (GLCNAC. . .) (POTENTIAL).

POTENTIAL.

NEUTROPSIN.
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT	TURN	118	119
FT	STRAND	122	126
FT	STRAND	140	141
FT	TURN	148	149
FT	STRAND	151	156
FT	STRAND	170	170
FT	STRAND	172	178
FT	HELIX	181	187
FT	TURN	189	191
FT	TURN	194	195
FT	STRAND	196	200
FT	TURN	202	203
FT	STRAND	206	206
FT	TURN	209	210
FT	TURN	212	213
FT	STRAND	215	218
FT	TURN	219	220
FT	STRAND	221	228
FT	STRAND	235	235
FT	TURN	236	237
FT	STRAND	238	238
FT	STRAND	240	244
FT	HELIX	245	256
SQ	SEQUENCE	260 AA;	BESF6FE8B37CD60E CRC64;
Query Match 45.9%; Score 698.5; DB 1; Length 260;			
Best Local Similarity 52.0%; Pred.No. 1.8e-56;			
Matches 129; Conservative 35; Mismatches 77; Indels 7; Gaps 3			
Oy	39	ILLALATGNGETR-----IIKPECKPHSQPOMALTEKRRLCGATLIAPRWLLTAA	93
Dd	13	ILLLFLPMAMALTLTAQSGSKILEGRCLIPHSQPWQALFOGERLLCGVAVGVDRWLTTAA	72
Oy	94	HCLKERYIVHGOHLLOKEEGCEQTRTATESPPHPGFNNSLPKDHNDIMLVKMSPVS	153
Dd	73	HCKKQKYEVRLGDHLSQRDPEGEIQVAQSIOHPCTYNSNP-EDSHIMILIRLONSAN	131
Oy	154	ITWAVRPPLTSSRCVTAGTSCLISGWSTSSPOLRLPHTLRCANITIIEBKCCENAYPSN	213
Dd	132	LGDKKVPOLANLCPRVGOKCIISGMGTVTSPOENPNPTLNCAEVKIYSQNKCERAYPGK	191
Oy	214	ITDTMVACSVDEGGKSDSCGDSGGLVCYNQSLGGIISWGODPCAITRKRGVTVKVKYYD	273
Dd	192	ITEGWCAG-SSENGADTCOGDGGPLVCDGMLDGITWSGSDPGCKPEKGVVYTKICRYTT	250
Oy	274	WIOETMKN	281
Dd	251	WIKKTMDN	258
RESULT 5			
ID	KLKF_HUMAN	STANDARD:	PRT: 256 AA.
AC	Q9H2R5; Q15358; Q9H2R3; Q9H2R4; Q9H2R6; Q9HBG9;		
DT	16-OCT-2001 (Rel. 40; Created)		
DT	16-OCT-2001 (Rel. 40; Last sequence update)		
DT	28-FEB-2003 (Rel. 41; Last annotation update)		
DE	Kallikrein 15 precursor (EC 3.4.21.-) (ACO protease).		
GN	KLK15.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	(1)		
RP	SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.		
RX	PubMed=11010966;		
RX	Youset G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;		
RA	"Molecular cloning of the human kallikrein 15 gene (KLK15). Up-		
RT	regulation in prostate cancer";		
RL	J. Biol. Chem. 276:53-61(2001).		
RN	(2)		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20510030; PubMed=11054574;		

[illegible]


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FT ACT SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 39 173 BY SIMILARITY.
FT DISULFID 58 74 BY SIMILARITY.
FT DISULFID 145 246 BY SIMILARITY.
FT DISULFID 152 218 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 208 233 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 23 23 A -> AACGSLDLTLTYANLPCVHLNPMQPSGHCRCRG
WRSNLPDPPA (in isoform 2).
SQ SEQUENCE 260 AA; 28048 MW; EF4395E5B8C3E660 CRC64;

Query Match 45.3%; Score 690; DB 1; Length 260;
Best Local Similarity 49.2%; Pred. No. 1.1e-55;
Matches 125; Conservative 45; Mismatches 80; Indels 4; Gaps 3;

QY 26 RSSPLQAMRLIQLIL-ALATGLVGEETRIINGFECKPHSOPMOALFEKTRLLCGATL 83
DB 3 RPRPRAAKTMWFLLLGAMWAGHSRAOEDKVLGHCQPHSQWQALLFGQGLCGVIL 62
QY 84 IAPRWLLTAHCLKPRYIYHLGOHNLQKEEGCQRTTATESFPHPGFNNSLPNKDRNDI 143
DB 63 VGGNWWLTAHCKKPKYTVRLGDHSLQNKDGPQEIIPVQSIHPPCYNSS-DVEDHNHDL 121
QY 144 MLVKMASPVISITAVRPLTLSSRCVATGSSCLISGMSGTSSPOLRLPHLRCAANTITIEH 203
DB 122 MLQLQLDQASLGSKVPRISLADCTOPGQKCTVSGWGTVSPENPDLNCEVAKIPFO 181
QY 204 OKCENAYPGNITPTWVCASVOEGSGDCSGSGPVCVNCOSLOGIISWGODPCAIRRRKG 263
DB 182 KCGEDAYPGQITDGMWCAGSSKGA-DTCGDSGGLVCGALOGITMSGSDPCGRSDKRG 240
QY 264 VYTKVCKYVDWIOE 277
DB 241 VYTNICRYLDWIKK 254

RESULT 7
KLLKD HUMAN STANDARD; PRT; 277 AA.
ID KLLKD HUMAN 09UKR3; Q9Y433;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)
GN KLLK13 OR KLLK14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCB1_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=20229789; PubMed=10766816;
RA Yousef G.M., Chang A., Diamandis E.P.;
RT "Identification and characterization of KLK-14, a new kallikrein-like
RT gene that appears to be down-regulated in breast cancer tissues.";
RL J. Biol. Chem. 275:11891-11898(2000).

(2)
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez W., Stilaagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
RA Danganan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andeise T., Tranheim M., Altix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carraro A.V.;
RT "Sequence analysis of chromosome 19q13.4.";
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.

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RP SEQUENCE OF 1-180 FROM N.A.
RC TISSUE-Uterus;
RA Ansoyge W., Wikner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, BREAST, TESTIS AND
CC SALIVARY GLAND.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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DR EMBL; AF135024; AAD26425.2; -
DR EMBL; AC011473; AAG23259.1; -
DR EMBL; AL050220; CAB43320.1; ALT_INIT.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.306; -.
DR Genew; HGNC:6361; KLK13.
DR MIM; 605505; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005576; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR001254; Ser_protease_fam.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00020; TRYP_SP; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Serine protease; Glycoprotein; Signal.
FT SIGNAL 1 16
FT CHAIN 17 277
FT ACT_SITE 76 76 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 124 124 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 218 218 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 42 178 BY SIMILARITY.
FT DISULFID 61 77 BY SIMILARITY.
FT DISULFID 157 224 BY SIMILARITY.
FT DISULFID 189 203 BY SIMILARITY.
FT DISULFID 214 239 BY SIMILARITY.
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 170 180 VNYPTLQCAN -> GMHPHRWPEAP (IN REF. 3).
SQ SEQUENCE 277 AA; 30570 MW; BA8A9E8DCFB5D542 CRC64;

Query Match 45.1%; Score 687.5; DB 1; Length 277;
Best Local Similarity 48.5%; Pred. No. 1.9e-55;
Matches 126; Conservative 48; Mismatches 71; Indels 15; Gaps 3;

QY 36 LQILALATGLVGG---ETRIK-----GFECKPHSOPMOALFEKTRLLCGA 81
DB 4 LALVALASLTLLALSGVSGSSKVLNTNGSGLPBGYTCFPHSQWQALLVQGNLLCG 63
QY 82 TLIAAPRWLLTAHCLKPRYIYHLGOHNLQKEEGCQRTTATESFPHPGFNNSLPNKDRNDI 141
DB 64 VLVHKKWVLTAAHCKKPKYTVRLGDHSLQNKDGPQEIIPVQSIHPPCYNSS-DVEDHNHDL 123
QY 142 MLVKMASPVISITAVRPLTLSSRCVATGSSCLISGMSGTSSPOLRLPHLRCAANTITIEH 200
DB 124 DIMLELDSPOVLGYIOTLPISHNNRLTPGTTCVSGWGTVSPENPDLNCEVAKIPFO 183
QY 201 IEHOKCENAYPGNITPTWVCASVOEGSGDCSGSGPVCVNCOSLOGIISWGODPCAIRRRKG 260
DB 184 RSDERCQVYVGKLTIDNMLCGATGKREGSGDCSGSGPVCVNCOSLOGIISWGODPCGQPD 243
QY 261 KPGVYTKVCKYVDWIOETMK 280
DB 244 RPYVTVRSRYVLMIRETIR 263

```

RESULT 8	KLK5_HUMAN	STANDARD:	PRT;	293 AA.
ID	KLK5_HUMAN			
AC	O9Y337; O9HBG8;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)			
DE	(Kallikrein-1like protein 2) (KLK-12).			
GN	KLK5 OR SCFE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	TISSUE=Stratum corneum;			
RX	MEDLINE=99445563; PubMed=10514489;			
RX	Brattsand M., Egelund T.;			
RT	"Purification, molecular cloning, and expression of a human stratum			
RT	corneum trypsin-like serine protease with possible function in			
RT	desquamation.";			
RL	J. Biol. Chem. 274:30033-30040(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20118156; PubMed=10652563;			
RX	Yousef G.M., Luo L.-Y., Diamandis E.P.;			
RT	"Identification of novel human kallikrein-like genes on chromosome			
RT	19q13.3-q13.4.";			
RL	Anticancer Res. 19:2843-2852(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20510030; PubMed=11054574;			
RX	Gan L., Lee J., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,			
RA	Moss P., Paeppe B., Wang K.;			
RT	"Sequencing and expression analysis of the serine protease gene			
RT	cluster located in chromosome 19q13 region.";			
RL	Gene 257:119-130(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Ovary;			
RX	MEDLINE=22388257; PubMed=12477932;			
RX	Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buerckel K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,			
RA	Rosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Boak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faney U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blaesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,			
RA	Schmerch A., Schain J.E., Jones S.J.W., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-1- FUNCTION: MAY BE INVOLVED IN DESQUAMATION.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN SKIN, BREAST, BRAIN AND TESTIS.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.			
CC	-----			
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DR      EMBL; AF168768; AAF03101.1; -
DR      EMBL; AF153028; AAD26429.1; -
DR      EMBL; AF243527; AAG33358.1; -
DR      EMBL; BC008036; AAH08036.1; -
DR      HSSP; P00763; IDPO.
DR      MEROPS; S01.017; -
DR      Genew; HGNC:6366; KLU5.
DR      MIM; 605643; -
DR      GO; GO:0005615; C:extracellular space; TAS.
DR      GO; GO:0008544; P:epidermal differentiation; TAS.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR      InterPro; IPR001314; Chymotrypsin.
DR      InterPro; IPR001254; Ser_protease_Try.
DR      Pfam; PF00089; trypsin; 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      SMART; SM00020; TRYPSIN_DOM; 1.
DR      PROSITE; PS50240; TRYPSIN_HIS; 1.
DR      PROSITE; PS00135; TRYPSIN_SER; 1.
KW      Hydroxylase; Serine protease; Glycoprotein; Signal.
FT      SIGNAL          1      22
FT      CHAIN           23      293
FT      ACT_SITE       108      108
FT      ACT_SITE       153      153
FT      ACT_SITE       245      245
FT      DISULFID        73      206
FT      DISULFID        93      109
FT      DISULFID       178      279
FT      DISULFID       185      251
FT      DISULFID       217      231
FT      DISULFID       241      266
FT      CARBOHYD        69      69
FT      CARBOHYD       173      173
FT      CARBOHYD       208      208
FT      CARBOHYD       252      252
FT      COMFLICT        25
FT      SEQUENCE       293 AA;  D92C92F5609B5946 CRC64;
Query Match      42.7%; Score 650.5; DB 1; Length 293;
Best Local Similarity 50.6%; Pred. No. 4.8e-52;
Matches 118; Conservative 41; Mismatches 67; Indels 7; Gaps 4
OY      52      TRIIKGFCKRSHSPWQNA-LFEKTRILCGATLIAPRWLLTAAACLKRYIVHLCQNHQ 110
DB      65      SRIINGSCDMDHTQWPQMAALLRPQLYCGALVHNPQLLTAHCRKRYFVRLRLHYSLS 124
OY      111     K-EEGCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPVSTIWAVRPLTUSRCVT 169
DB      125     PYVESGGQMPQGVKXSIHPHGYX---HPGHSNDMLILKLNRIIRPTKQVRPIINVSHPCS 180
OY      170     AGTSLGISWMSSTSPQLRLPHTRLCANITITIIHOKGCENALPFGNITDTPMVCASVDEGKD 229
DB      181     AGTKCLVSGWGQTTSPPQVHFPRKVLQCLNLSVLSQKRCEDAPRQIDDTMPCAG-DKAGR 239
OY      230     SCQSGSGGPLYCNCNOSLOGIISMGDPCATITKPPGYTVTKCYKVDIMQETMKN 282
DB      240     SCQSGSGGSPVVCNCSLOGVSWGDIYPCARPRPRPVYTNLCKFTKMIQIETIQAN 292
-----
RESULT 9
KLUKE_HUMAN
ID      KLUKE_HUMAN      STANDARD;      PRT;      251 AA.
AC      Q9P0G3;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like protein 6)
DE      (KIK-16)
DE      KLUK4 OR KLUK6.
GN      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yousef G.M., Diamandis E.P.;
 RT "Molecular characterization, mapping, and tissue expression of KLK16,
 a hormonally regulated kallikrein-like gene.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
 RX MEDLINE=21250997; PubMed=11352573;
 RA Hooper J.D., Bul L.T., Rae F.K., Harvey T.J., Myers S.A.,
 RA Ashworth L.K., Clements J.A.;
 RT "Identification and characterization of KLK14, a novel kallikrein
 serine protease gene located on human chromosome 19q13.4 and expressed
 in prostate and skeletal muscle.";
 RL Genomics 73:117-122(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
 RA Dangnan L., Eller A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andeise T., Tranheim M., Altix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carraro A.V.;
 RT "Sequence analysis of chromosome 19q13.4.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20545474; PubMed=10969073;
 RA Harvey T.J., Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L.K.,
 RA Clements J.A.;
 RT "Tissue-specific expression patterns and fine mapping of the human
 kallikrein (KLK) locus on proximal 19q13.4.";
 RL J. Biol. Chem. 275:37397-37406(2000).
 CC [1] SUBCELLULAR LOCATION: Secreted (Probable).
 CC [2] TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, BONE MARROW AND
 CC FETAL LIVER. ALSO EXPRESSED IN LIVER, PANCREAS, FETAL SPLEEN,
 CC PROSTATE AND SKELETAL MUSCLE.
 CC [3] SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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 CC -----
 DR EMBL: AF161221, AAD50773.2; -;
 DR EMBL: AF283669, AAK48523.1; -;
 DR EMBL: AF283670, AAK48524.1; -;
 DR EMBL: AC011473, AAG23260.1; -;
 DR HSSP: P00763, IDPO.
 DR MEROPS: S01.029; -;
 DR GeneW: HGNC:6362; KLK14.
 DR MIM: 606135; -;
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00069; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM0020; Tryp_SPC_1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolase, Serine protease, Signal, Zymogen.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 251
 KALLIKREIN 14.

FT ACT SITE 67 67 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 111 111 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 31 164 BY SIMILARITY.
 FT DISULFID 52 68 BY SIMILARITY.
 FT DISULFID 143 210 BY SIMILARITY.
 FT DISULFID 175 189 BY SIMILARITY.
 FT DISULFID 200 225 BY SIMILARITY.
 SQ SEQUENCE 251 AA; 27452 MW; 9087953BAFA7ED25 CRC64;
 Query Match 41.5%; Score 632.5; DB 1; Length 251;
 Best Local Similarity 47.6%; Pred. No. 1.8e-50;
 Matches 118; Conservative 42; Mismatches 81; Indels 7; Gaps 3;
 QY 36 LQILALATGAVGSETRIKPECKPHSQPQALF--EKTRLCATLTPRLTLTA 93
 DB 8 LQVLAIAM-TQSQEDENKXIGCHTTRSSQPMQALLAGPRRRFLCGGLLSGOWITAA 66
 QY 94 HCLKPRYIVHGOHNLQKEGCEGOTRTATSPHPGPNNSLPNKDHRNDIMLVKASPV 153
 DB 67 HCGRPILQVALGKHLNRWEATQVLRVROVTHENVN---SRTHNDMLLQLOQPAR 122
 QY 154 ITMAVRPLTLSSRCVYTAGTSCDISGSGTSSPOLRPLTLRCANITIEHQECENAYPN 213
 DB 123 IGRAVRPIEVTDQACASPGTSCVSGMTISSPIARYPASLQCVNINISPDVCQKAYPT 182
 QY 214 ITDITWVCAVSVDGSGDCSCGDSGGLVNCQSLQGIISWQDPCATRKRGVTKCKRYD 273
 DB 183 ITPGNVCAGVPGGKDSQCGSGGLVCRQGLQGLVSGMERCALPGYGVYTNLCYRS 242
 QY 274 WIOETMKN 281
 DB 243 WIEETMRD 250
 RESULT 10
 KKC HUMAN STANDARD; PRT; 248 AA.
 ID KKC HUMAN
 AC QYUKR0, QYUKR1; 40. Created
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)
 DE (KIK-15).
 GN KLK12 OR KLK15.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20118156; PubMed=10652563;
 RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
 RT "Identification of novel human kallikrein-like genes on chromosome
 RT 19q13.3-q13.4.";
 RL Anticancer Res. 19:2843-2852(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Yousef G.M., Maglilara A., Scortilas A., Diamandis E.P.;
 RT "Cloning of new alternatively spliced forms of the kallikrein-like
 RT gene 5 (KIK-15).";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Paepier B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,

RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
 RA Dandapani L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andriase T., Tranheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Duare S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.,
 RT "Sequence analysis of chromosome 19q13.4."
 RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9UKR0-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9UKR0-2; Sequence=VSP_005403;
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL, AF135025; AAD26426.2; -;
 CC EMBL, AF135025; AAF06065.1; -;
 CC EMBL, AF243527; AAG33365.1; -;
 CC EMBL, AC011473; AAG23258.1; -;
 CC HSSP, P00763; IDPO.
 CC MEROPS, S01.020; -;
 CC GeneW, HGNC:6360; KLM12.
 CC MIM, 605539; -;
 CC GO: GO:0005576; C:extracellular; NAS.
 CC GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
 CC InterPro: IPR001254; Ser:protease_Try.
 CC DR Pfam: PF00089; trypsin; 1.
 CC DR SMART, SM00020; TRYP_SPC; 1.
 CC DR PROSITE, PS50240; TRYP_SIN_DOM; 1.
 CC DR PROSITE, PS00134; TRYP_SIN_HIS; 1.
 CC DR PROSITE, PS00135; TRYP_SIN_SER; 1.
 CC KW Hydrolase, Serine protease; Glycoprotein; Signal;
 CC Alternative splicing.
 CC FT SIGNAL 1 17
 CC FT CHAIN 18 248
 CC FT ACT_SITE 62 62 KALLIKREIN 12.
 CC FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT DISULFID 28 161
 CC FT DISULFID 47 63 BY SIMILARITY.
 CC FT DISULFID 133 235 BY SIMILARITY.
 CC FT DISULFID 140 206 BY SIMILARITY.
 CC FT DISULFID 172 186 BY SIMILARITY.
 CC FT DISULFID 196 222 BY SIMILARITY.
 CC FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPLIC 236 248 KYVDWIRMIMRN -> NSTVLGLTSMNFCQPF (1n isoform 2).
 CC /FTId=VSP_005403.
 CC SEQUENCE 248 AA; 26733 MW; BB473B98FBAF03 CRC64;
 CC Query Match 40.6%; Score 618.5; DB 1; Length 248;
 CC Best Local Similarity 48.2%; Pred. No. 3.3e-49;
 CC Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;
 CC
 CC QY 36 LQILLALATGVGGET-RIIKGFCKPHSQWQALPFKTLGLLCATLIARMLITAAH 94
 CC DB 3 LSIIFLLCVLGSQAATPKIFNGTEGKRSQPMQVGLFEGTSLRCGVLIIDHRWLITAAH 62
 CC QY 95 CLKPRIYVHLGOHNLQKEGCEQTRTATSPFHPGFNNLSLPKDRNDIMLVKMASPSI 154
 CC DB 63 CGSGRTWRLGSHLSQLDWTQIIRHSGSVTHPGLGA--STSHEDRLRLRLPLPRV 120

QY 155 TWAVRPLTLSSRCVYTAGTSCILSGWSTSSPOLRLPHTLRCAANTIIIEHOKENAYPGNI 214
 DB 121 TSSVQPLPLPNDCAITAGTCHVSQGIINHRNFPDLQCLNLSIVSHATCHGVPGRI 180
 QY 215 TDTWVCASVQSGKDCGSGGSPLYCQSLQGIISWQD-PPCALTRPGYTVKVCXYD 273
 DB 161 TSNMVCAG-GVPGQDAGCGDSGGLVCGVLQGLVSWGSGVPGCGDGIIPGYITIICTYD 239
 QY 274 WIOETMKNN 282
 DB 240 WIRMIMRN 248
 CC
 CC RESULT 11
 CC KLT7 RAT STANDARD; PRT; 261 AA.
 CC ID KLT7 RAT
 CC AC P36373;
 CC DT 01-UN-1994 (Rel. 29, Created)
 CC DT 01-UN-1994 (Rel. 29, Last sequence update)
 CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
 CC DE Glandular kallikrein 7, submandibular/renal precursor (EC 3.4.21.35)
 CC DE (Tissue kallikrein) (RKG-7) (RSKG-7) (Esterase B) (Proteinase A).
 CC GN KLT7 OR KLT-7
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OG Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 CC OX NCBI_TaxId=10116;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=8908074; PubMed=2849988;
 CC RA Chen Y.-P., Chao J., Chao L.;
 CC RT "Molecular cloning and characterization of two rat renal kallikrein
 CC genes.";
 CC RT Biochemistry 27:7189-7196(1988).
 CC RL [2]
 CC RN [2]
 CC RP SEQUENCE OF 25-75.
 CC RC TISUB=Submaxillary gland;
 CC RX MEDLINE=88198057; PubMed=3482210;
 CC RA Kato H., Nakamishi E., Enyoji K., Hayaishi I., Oh-Ishi S., Iwanaga S.;
 CC RT "Characterization of serine proteinases isolated from rat
 CC submaxillary gland: with special reference to the degradation of rat
 CC kininogens by these enzymes".
 CC RT J. Biochem. 102:1389-1404(1987).
 CC RL [3]
 CC CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS
 CC IN KININOGEN TO RELEASE LYS-BRADYKININ.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in
 CC small molecule substrates. Highly selective action to release
 CC kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of
 CC Met-|-Xaa or Leu-|-Xaa.
 CC CC -1- TISSUE SPECIFICITY: KIDNEY AND SUBMANDIBULAR GLAND.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC EMBL, M19647; AAA41461.1; -;
 CC DR PIR, A31136; A31136.
 CC DR HSSP, P00759; ITON.
 CC DR MEROPS, S01.406; -;
 CC InterPro: IPR001254; Ser:protease_Try.
 CC Pfam, PF00089; trypsin; 1.
 CC SMART, SM00020; TRYP_SPC; 1.
 CC PROSITE, PS50240; TRYP_SIN_DOM; 1.
 CC PROSITE, PS00134; TRYP_SIN_HIS; 1.
 CC PROSITE, PS00135; TRYP_SIN_SER; 1.
 CC KW Hydrolase, Serine protease; Glycoprotein; Multigene family; Zymogen;
 CC Signal.

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FT SIGNAL 1 18 PROBABLE.
FT PROPP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 261 GLANDULAR KALLIKREIN 7,
FT ACT_SITE 65 65 SUMANDIBULAR/RENAL.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.
FT ACT_SITE 213 213 CHARGE RELAY SYSTEM.
FT DISULFID 31 173 BY SIMILARITY.
FT DISULFID 53 66 BY SIMILARITY.
FT DISULFID 152 219 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 209 234 BY SIMILARITY.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 35 35 S -> D (IN REF. 2).
FT CONFLICT 46 46 T -> S (IN REF. 2).
SQ SEQUENCE 261 AA; 28972 MW; 4FB06C422F25A616 CRC64;

Query Match 40.6%; Score 618.5; DB 1; Length 261;
Best Local Similarity 44.5%; Pred. No. 3.5e-49;
Matches 114; Conservative 45; Mismatches 86; Indels 11; Gaps 2;

QY 38 LILALATGIVC---GFTRIIGFECRPHSQWQALFEKTRLLCGATLIAPRLTLTA 93
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 5 ILFLDLISLQIDAPPGOSRIVIGYCKCKNSQCPWQVALYSFTYLCGVLIIDPSWVITAA 64
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 94 HCLKPRYIVHLGOHNLQKRGCEQRTATSESPHPENNSL-----PNKQHRNDIMLV 146
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 65 HCSNNYQWVLGNHNLLEDPFQPHLVSGSPHPYKPKPLKRNHTRKRGDHSNDMLL 124
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 147 KMASPVSTMAVAPLTLSSRCVACTSCULISGWSTSSPOLRLPHTLRGANITIEHQK 206
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 125 HUSQPADITDGVAVIDLPTREPRKVGSTCLASGSKTRKPLIWERPDQLQCVNHLISNEKC 184
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 207 ENAYPGNITDTMVCASVQSGKSDCCGDSGSPVNCOSLOGITISWQDPCATIRKPGVYT 266
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 185 IKAYPEKIVDMLCAELBEGSKDTCGDSGGLICDGVLIQITISGVSVCATKTNMFAIYT 244
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 267 KVCKYVDWIOETMKNN 282
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 245 KLIKFTSWIKWEKEN 260
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
KLIK1_RAT STANDARD; PRT; 261 AA.
ID KLIK1_RAT
AC P00758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glandular kallikrein, pancreatic 1 precursor (EC 3.4.21.35) (Tissue
DE kallikrein) (PS kallikrein) (RGR-1).
GN KLIK1 OR KLIK-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
   (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=83117659; PubMed=6961406;
RA Swift G.H., Dagorn J.-C., Ashley P.L., Cummings S.W., McDonald R.J.;
RT "Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid
RT sequence of the encoded preproenzyme."
RL Proc. Natl. Acad. Sci. U.S.A. 79:7263-7267(1982).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Submaxillary gland;
RX MEDLINE=86051477; PubMed=2998455;
RA Ashley P.L., Macdonald R.J.;
RT "kallikrein-related mRNAs of the rat submaxillary gland: nucleotide
RT sequences of four distinct types including tonin."
RL Biochemistry 24:4512-4520(1985).
RN (3)
RP SEQUENCE FROM N.A.

```

```

RC TISSUE=Kidney;
RX MEDLINE=89327211; PubMed=2753879;
RA Inoue H., Fukui K., Miyake Y.;
RT "Identification and structure of the rat true tissue kallikrein gene
RT expressed in the kidney."
RL J. Biochem. 105:834-840(1989).
RN (4)
RP SEQUENCE FROM N.A.
RX MEDLINE=89214217; PubMed=2708383;
RA Wines D.R., Brady J.M., Pritchett D.B., Roberts J.L., Macdonald R.J.;
RT "Organization and expression of the rat kallikrein gene family."
RL J. Biol. Chem. 264:7653-7662(1989).
RN (5)
RP SEQUENCE OF 48-261 FROM N.A.
RX MEDLINE=86131678; PubMed=3004582;
RA Gerald W.L., Chao J., Chao L.;
RT "Immunological identification of rat tissue kallikrein cDNA and
RT characterization of the kallikrein gene family."
RL Biochim. Biophys. Acta 866:1-14(1986).
CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS
CC IN KININOGEN TO RELEASE LYS-BRADYKININ.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-Xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of
CC Met-Xaa or Leu-Xaa.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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CC -----
DR EMBL, J00758; -; NOT ANNOTATED CDS.
DR EMBL, M1563; AAA41464.1; ALT_INIT.
DR EMBL, M23876; AAA41462.1; JOINED.
DR EMBL, M23874; AAA41462.1; JOINED.
DR EMBL, M23875; AAA41462.1; JOINED.
DR EMBL, D00448; BAA00346.1; ALT_INIT.
DR EMBL, D00446; BAA00346.1; JOINED.
DR EMBL, D00447; BAA00346.1; JOINED.
DR EMBL, X03560; CAA27247.1; -.
DR PIR, A00944; KORTP.
DR HSSE, P00757; ISGF.
DR MEROPS, S01.405; -.
DR InterPro: IPR001254; Ser. protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR SMART, SM00020; Tryp_Sec; 1.
DR PROSITE, PS50240; TRYPsin_DOM; 1.
DR PROSITE, PS00134; TRYPsin_HIS; 1.
DR PROSITE, PS00135; TRYPsin_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;
KW Signal.
FT SIGNAL 1 18 PROBABLE.
FT PROPP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 261 GLANDULAR KALLIKREIN 1.
FT ACT_SITE 112 261 CHAIN 1.
FT ACT_SITE 65 65 CHAIN 2.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.
FT ACT_SITE 213 213 CHARGE RELAY SYSTEM.
FT DISULFID 31 173 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 152 219 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT CARBOHYD 209 234 BY SIMILARITY.
FT CONFLICT 108 108 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 261 AA; 28852 MW; F2P99C0227A7882B CRC64;

Query Match 40.5%; Score 617.5; DB 1; Length 261;
Best Local Similarity 43.8%; Pred. No. 4.3e-49;

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RESULT 13			
TRY3_CHICK	STANDARD;	PRT;	248 AA.
AC	Q90629;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Trypsin II-P29 precursor (EC 3.4.21.4).		
OS	Gallus gallus (Chicken)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauiria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Pancreas;		
RX	MEDLINE=95251611; PubMed=7733865;		
RA	Wang K., Gan L., Lee I., Hood L.E.;		
RT	"Isolation and characterization of the chicken trypsinogen gene		
RT	family ";		
RL	Biochem. J. 307:471-479(1995).		
CC	- - CATALYTIC ACTIVITY: Preferential cleavage: Arg- -Xaa, Lys- -Xaa.		
CC	- - SUBCELLULAR LOCATION: Extracellular.		
CC	- - TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE PANCREAS WHILE		
CC	LOWER LEVELS ARE FOUND IN THE LIVER, SPLEEN AND THYMUS.		
CC	- - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; U15157; AAA79914.1; -.		
DR	PIR; S55066; S55066.		
DR	HSSP; P00763; IDPO.		
DR	MEROPS; S01.151; -.		
DR	InterPro; IPR001254; Ser.protease_Try.		
DR	Pfam; PF00089; trypsin.1.		
DR	SMART; SM00020; Tryp.Spec.1.		
DR	PROSITE; PS0240; TRYPsin_DOM. 1.		
DR	PROSITE; PS00134; TRYPsin_HIS. 1.		
DR	PROSITE; PS00135; TRYPsin_SER. 1.		
KW	Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;		
KW	Multigene family.		
FT	SIGNAL	1	16
FT	PROPEP	17	25
FT	CHAIN	26	248
			BY SIMILARITY.
			ACTIVATION PEPTIDE (BY SIMILARITY).
			TRYPsin II-P29.

FT	ACT SITE	65	65	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT SITE	109	109	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT SITE	202	202	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	DISULFID	32	162	BY SIMILARITY.
FT	DISULFID	50	66	BY SIMILARITY.
FT	DISULFID	134	235	BY SIMILARITY.
FT	DISULFID	141	208	BY SIMILARITY.
FT	DISULFID	173	187	BY SIMILARITY.
FT	DISULFID	198	222	BY SIMILARITY.
FT	SITE	196	196	REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ	SEQUENCE	248 AA;	26622 MW;	ESB16B07622B588E CRC64;
Query Match	Similarity	40.2%;	Score 612;	DB 1; Length 248;
Best Local	Similarity	48.2%;	Pred. No. 1.3e-48;	
Matches 121;	Conservative	38;	Mismatches 82;	Indels 10; Gaps 5;
Qy	33	MRIOLIL--LALTLGLVG--ETRIIKGFECRHPSPOMQALFEKTRLLCGATLIAPRW	88	
Db	1	MKFLFLILSCGAAVAPFGGADDDKICGYGTCRPHSNVPYQSL-NSGVHFGGSLNSQW	59	
Qy	89	LITAAHCLKRPYIVHLGQHNIOKEEGEGQRTFATESPPHGFNNLSLPKXDRNDIMLVKM	148	
Db	60	VLSAAHCKYRSIQRLTEYVNDIVQDESEVWSSVITIRHPKXSITLTN---NDIMILKL	115	
Qy	149	ASPSITMAVAPRLTLRSRCYTAGTSCILSGMGSTSSPOLRLPHILRCANITIIHQKEN	208	
Db	116	ASAEVSYADSDIOPIALPSSCAVAGTECLISGNGTLNSGVNYPELLQCNADILSDQEOE	175	
Qy	209	AYPQINIDTWACAVQGGKSDCCGGSGGPIVNCOSHYGISTMGQDPICATRRKPGVYTKV	268	
Db	176	AYPGDITSNMTCVFLEGGKSDCCGGSGGPIVNCGEILOGIVSKGIG-CALKGYGCVYTKV	234	
Qy	269	CKYVDWIOETM	279	
Db	235	CNYVDWIOETI	245	
RESULT 14	KLKC_RAT	STANDARD;	PRT;	259 AA.
ID	KLKC_RAT	P36376;		
AC	01-JUN-1994	(Rel. 29, Last sequence update)		
DT	01-JUN-1994	(Rel. 29, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Glandular kallikrein 12, submandibular/renal precursor (EC 3.4.21.35)			
DE	(Tissue kallikrein) (RSKG-3).			
OS	KLK12 OR KLK-12.			
NS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridi; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89088074; Pubmed=2849988;			
RA	Chen Y.-P., Chao J., Chao L.,			
RT	"Molecular cloning and characterization of two rat renal kallikrein			
RT	genes."			
RL	Biochemistry 27:7189-7196(1988).			
CC	- FUNCTION: GLANDULAR KALLIKREIN CLEAVE MET-LYS AND ARG-SER BONDS			
CC	IN KININOGEN TO RELEASE LYS-BRADYKININ			
CC	- CATALYTIC ACTIVITY: Preferential cleavage of Arg- -Xaa bonds in			
CC	small molecule substrates. Highly selective action to release			
CC	kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of			
CC	Met- -Xaa or Leu- -Xaa.			
CC	- TISSUE SPECIFICITY: KIDNEY AND SUBMANDIBULAR GLAND.			
CC	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/)			

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or send an email to license@isb-sib.ch).
CC EMBL: M19648; AAA51640.1; -.
DR EMBL: M22922; AAA51640.1; JOINED.
DR PIR: B31136; B31136.
DR HSSP: P00759; ITON.
DR MEROPS: S01.160; -.
DR InterPro: IPR001254; Ser protease_Try.
DR Pfam: PF00089; trypsin_1.
DR SMART: SM00020; Tryp_Spc_1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;
KM Signal.
FT SIGNAL 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 259 SUBMANDIBULAR/RENAL.
FT ACT_SITE 63 63 CHARGE RELAY SYSTEM.
FT ACT_SITE 118 118 CHARGE RELAY SYSTEM.
FT DISULFID 211 211 CHARGE RELAY SYSTEM.
FT DISULFID 31 171 BY SIMILARITY.
FT DISULFID 48 64 BY SIMILARITY.
FT DISULFID 150 217 BY SIMILARITY.
FT DISULFID 182 196 BY SIMILARITY.
FT DISULFID 207 232 BY SIMILARITY.
FT CARBOHYD 91 91 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 259 AA; 28759 MW; 535A8EE25435144F CRC64;

Query Match 40.2%; Score 611.5; DB 1; Length 259;
Best Local Similarity 43.4%; Pred. No. 1.5e-48;
Matches 112; Conservative 45; Mismatches 88; Indels 13; Gaps 3;

QY 36 LQILALATGLVG---GETRIKGFECRPHSQWQAALFEKTRLLCGATLIAPRWLT 91
DB 3 LQILFLVLSVRIDAPPGQSRVGVGKCEKNSQFWQAVI--NRYLGGVLIIDPSWVIT 60
QY 92 AAHCLKPRIVHLGQNLQKECECEOTRATESFFPHGPN-----NSLPKNDHRNDIM 144
DB 61 AAHCASHNHVLLGRNNLFKDEPFAPYRVVNSFPHPDYNPFPMKNHTLFPDSDHSDNDIM 120
QY 145 LVKMASPVITWAVRPLTSSRCVTAAGTSCISGWSGSSPQLRLPHTRCANITIIHQ 204
DB 121 LHLSPADITDGVKVIDLPTEBPXGSGTCLASGWSSTPLMEFPDDLCVNNITLSNE 180
QY 205 KCENAYPGNITDTMVCASVOEGGKDSQCGDSGGLVCNOSLOGIISWGDPCATRKPGV 264
DB 181 KCIKHTQWVTDMVLGAGLEGGKDTGNCNDSGGPLLCDGVLOGITSSWSPGGETNRPAI 240
QY 265 YTRKVCAYVDIQTMMKN 282
DB 241 YTRKLTFTSMIKVEMKEN 258

RESULT 15
KLK3_MOUSE
ID KLK3_MOUSE STANDARD; PRT; 261 AA.
AC P00756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glandular kallikrein K3 precursor (EC 3.4.21.35) (Tissue kallikrein)
DE (MGK-3) (7S nerve growth factor gamma chain) (Gamma-NGF).
GN KLK3 OR KLK-3 OR NGFG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=850716169; PubMed=6548955;

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RA Ullrich A., Gray A., Wood W.I., Hayflick J., Seeburg P.H.;
RT "Isolation of a cDNA clone coding for the gamma-subunit of mouse
RT nerve growth factor using a high-stringency selection procedure.";
RL DNA 3:367-392(1984).
(2)
RP SEQUENCE FROM N.A.
RX MEDLINE=85257431; PubMed=3848399;
RA Evans B.A., Richards R.I.;
RT "Genes for the alpha and gamma subunits of mouse nerve growth factor
RT are contiguous.";
RL EMBO J. 4:133-138(1985).
(3)
RP SEQUENCE OF 25-261.
RX MEDLINE=81264363; PubMed=7263706;
RA Thomas K.A., Baglan N.C., Bradshaw R.A.;
RT "The amino acid sequence of the gamma-subunit of mouse submaxillary
RT gland 7 S nerve growth factor.";
RL J. Biol. Chem. 256:9156-9166(1981).
(4)
RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
RC STRAIN=swiss webster; TISSUE=Submaxillary gland;
RX MEDLINE=98035451; PubMed=9351801;
RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;
RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
RT four binding proteins.";
RL Structure 5:1275-1285(1997).
CC -I- FUNCTION: 7S NGF ALPHA CHAIN STABILIZES THE 7S COMPLEX. THE BETA
CC DIMER PROMOTES NEURITE GROWTH. THE GAMMA CHAIN IS AN ARGININE-
CC SPECIFIC PROTEASE; IT MAY ALSO HAVE PLASMINOGEN ACTIVATOR
CC ACTIVITY, AS WELL AS MITOGENIC ACTIVITY FOR CHICK EMBRYO
CC FIBROBLASTS.
CC -I- CATALYTIC ACTIVITY: Preferential cleavage of Arg|-Xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of
CC Met|-Xaa or Leu|-Xaa.
CC -I- SUBUNIT: 7S NERVE GROWTH FACTOR IS COMPOSED OF TWO ALPHA CHAINS,
CC A BETA DIMER COMPOSED OF IDENTICAL CHAINS, AND TWO GAMMA CHAINS.
CC -I- MISCELLANEOUS: THIS PRECURSOR IS CLEAVED INTO SEGMENTS TO PRODUCE
CC THE ACTIVE FORM OF THE GAMMA CHAIN, WHICH OCCURS NATURALLY AS
CC COMBINATIONS OF EITHER TWO OR THREE SEGMENTS HELD TOGETHER BY
CC DISULFIDE BONDS: B1 + A OR B1 + C + B2.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, KALLIKREIN SUBFAMILY.
CC
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CC
CC EMBL: X01389; CAA25645.1; -.
CC EMBL: X01798; CAA25928.1; -.
CC EMBL: X01799; CAA25930.1; -.
CC PIR: A91005; NMSG.
CC PDB: 1SGF; 27-MAY-98.
DR MEROPS: S01.170; -.
DR MGD: MGI:97322; Ngfg.
DR InterPro: IPR001254; Ser protease_Try.
DR Pfam: PF00089; trypsin_1.
DR SMART: SM00020; Tryp_Spc_1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;
KM Signal; Growth factor; 3d-structure.
FT SIGNAL 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE.
FT CHAIN 25 261 GLANDULAR KALLIKREIN K3.
FT CHAIN 112 107 NERVE GROWTH FACTOR GAMMA CHAIN 1.
FT ACT_SITE 65 65 NERVE GROWTH FACTOR GAMMA CHAIN 2.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.

```

CHARGE RELAY SYSTEM.
N-LINKED (GLCNAC. . .).
SEGMENT B1.
SEGMENT A.
SEGMENT C.
SEGMENT B2.
MISSING (IN REF. 2).

FT ACT SITE 213 213
FT DISULFID 31 173
FT DISULFID 50 66
FT DISULFID 152 219
FT DISULFID 184 198
FT DISULFID 209 234
FT DISULFID 102 102
FT CARBOHYD 102 102
FT DOMAIN 25 107
FT DOMAIN 112 261
FT DOMAIN 112 164
FT DOMAIN 165 261
FT CONFLICT 108 111
FT STRAND 26 26
FT STRAND 29 30
FT HELIX 33 35
FT TURN 37 38
FT STRAND 39 44
FT STRAND 45 46
FT STRAND 47 56
FT TURN 57 58
FT STRAND 59 62
FT HELIX 64 66
FT STRAND 72 75
FT STRAND 79 79
FT TURN 80 81
FT TURN 85 86
FT STRAND 88 97
FT TURN 99 100
FT HELIX 103 105
FT TURN 118 119
FT STRAND 122 126
FT TURN 148 149
FT STRAND 151 156
FT STRAND 159 159
FT STRAND 167 167
FT STRAND 170 170
FT STRAND 172 179
FT HELIX 181 187
FT TURN 194 195
FT STRAND 196 200
FT STRAND 207 207
FT TURN 210 211
FT TURN 213 214
FT STRAND 216 219
FT TURN 220 221
FT STRAND 222 229
FT TURN 234 235
FT TURN 237 238
FT STRAND 241 245
FT HELIX 246 249
FT HELIX 250 258
FT TURN 259 259
SQ SEQUENCE 261 AA; 28998 MW; 4870748E174AF7C8 CRC64;

Query Match 40.2%; Score 611.5; DB 1; Length 261;
Best Local Similarity 43.0%; Pred. No. 1.5e-48;
Matches 110; Conservative 52; Mismatches 83; Indels 11; Gaps 2;

Qy 38 LILLALATGLVGG---ETRIIKGFECCKPHSOPQALFEKTRLLCGATLILAPRWLTPAA 93
Db 5 ILFLALSLGIDIAAPVQSRIVGFGFCKENSOQPMHVAVRYTQYLCGVLDPNMVLTAA 64
Qy 94 HCLKPRYIVHLGOHNIQKEGCEQTRTATESFPHPGFNNSLPNK-----DHRNDIMLV 146
Db 65 HCYDDNYKWLKGNLKFDEPSAQHRFVSKAIPHPGFNMSLMRKHIFLEVDYNDLMLL 124
Qy 147 KMAAPSVITWAVRPLTLSSRCTAGTSCILSGWGSTSSPOLRLPHTLRCAANTIIHOKC 206
Db 125 RLKSKPADITDVTVPITLPTPEEPKLSTCLASGWSITTPKFFQTDLDYCVNLKLPNEBC 184
Qy 207 ENAYPCNITDTWVCASVQEGKDSGCGSGPPLVCNOSLOGIISWGDPICALTRKPGVYT 266
Db 185 AKAHIEKVDNALCAGEMDGKDTCKGDSGGPLICDGVLOGITSMGHTPCGEPDMPGVYT 244

Qy 267 KVCXYVDNIQETMKNN 282
Db 245 KLNKFTSWIKDTMAKN 260

Search completed: October 22, 2003, 15:51:57
Job time : 10.935 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 15:48:57 ; Search time 35.319 Seconds
(without alignments)
2060.389 Million cell updates/sec

Title: US-09-856-320A-2
Perfect score: 1523
Sequence: 1 MORLRLRDMKSSGRGLTAA.....GVYTKVKYVDWIQETMKNN 282

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1332.5	87.5	275	4	Q8IXD7
2	1187	77.9	276	11	Q9QYN3
3	1129	74.1	249	11	Q9QYN4
4	692	45.4	260	4	Q8IWE9
5	685.5	45.0	255	4	Q96R00
6	683.5	44.9	254	11	Q8CGR4
7	678	44.5	276	11	Q8CGR6
8	665	43.7	251	11	Q9DB08
9	632	41.5	293	11	Q9D140
10	626	39.5	261	11	Q8CGR5
11	602	39.5	261	11	Q9JW70
12	600.5	39.4	246	11	Q921R9
13	599.5	39.4	234	11	Q9CV76
14	598.5	39.3	246	11	Q9K077
15	597.5	39.2	239	11	Q63275
16	597	39.2	246	11	Q9QUK9

17	592.5	38.9	261	6	Q9N1Q1
18	591.5	38.8	261	6	Q29474
19	587.5	38.6	235	11	Q63274
20	582	38.2	249	11	Q91VE3
21	576	37.8	263	11	Q9JW71
22	575	37.8	263	11	Q8QGW3
23	572.5	37.6	261	11	Q8C232
24	572	37.6	251	11	Q54854
25	570.5	37.5	263	11	Q9JW69
26	570.5	37.5	269	4	Q8IUS5
27	568.5	37.3	253	11	Q91Y82
28	568	37.3	246	11	Q88301
29	567.5	37.3	247	11	Q9CPN7
30	567	37.2	240	13	Q98TH0
31	566	37.2	245	13	Q82160
32	564.5	37.1	237	13	Q91515
33	563	37.0	247	13	Q42158
34	562	36.9	247	13	Q42608
35	561	36.8	247	11	Q9CPN9
36	560.5	36.8	253	4	Q885N9
37	560	36.8	244	13	Q42159
38	559	36.7	242	13	Q92039
39	558	36.6	254	6	Q9XSN6
40	556	36.5	238	13	Q9W7Q6
41	555.5	36.5	222	13	Q8AV11
42	553	36.3	243	13	Q8AV83
43	553	36.3	261	11	Q88309
44	552	36.2	242	13	Q9W7Q7
45	551	36.2	247	13	Q9W7Q5

ALIGNMENTS

RESULT 1	Q8IXD7	PRELIMINARY;	PRT;	275 AA.
AC	Q8IXD7			
DT	01-MAR-2003 (TRMBLrel. 23, Created)			
DT	01-MAR-2003 (TRMBLrel. 23, Last sequence update)			
DT	01-MAR-2003 (TRMBLrel. 23, Last annotation update)			
DE	Variant form hipostasin/KLK11.			
GN	KLK11.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Nakamura T., Mitsui S., Miki T., Yamaguchi N.;			
RT	"Molecular cloning and expression of a variant form of			
RT	hipostasin/KLK11 in prostate."			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB078780; BACS4105.1; "			
DR	SEQUENCE 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;			

Query Match	87.5%; Score 1332.5; DB 4; Length 275;
Best Local Similarity	90.9%; Pred. No. 3.9e-130;
Matches 250; Conservative	0; Mismatches 0; Indels 25; Gaps 1;
QY	33 MRIDLLALATGIVGGETRIIKGFCKPHSOPQOALFEKTRLLCGATLIAPWLTLTA 92
DB	1 MRIDLLALATGIVGGETRIIKGFCKPHSOPQOALFEKTRLLCGATLIAPWLTLTA 60
QY	93 AHCLKP-----RYIVHLGQNLQKEGCEQRTATESPPI 127
DB	61 AHCLKPWSLSPHVSFDDSSNVCLSHLSRIYVHLGQNLQKEGCEQRTATESPPI 120
QY	128 PGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTLSSRCVTAGTSCILSGSGTSSPOL 187
DB	121 PGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTLSSRCVTAGTSCILSGSGTSSPOL 180

QY 188 RLPHILRCANITIIIEHOKENAVPGNITDTWVCASVOEGKDCSGDSCGPIVNCOSLOG 247
 DB 181 RLPHILRCANITIIIEHOKENAVPGNITDTWVCASVOEGKDCSGDSCGPIVNCOSLOG 240
 QY 248 IISWGODPCATRKPGVYTKVKYVDMIOETMKN 282
 DB 241 IISWGODPCATRKPGVYTKVKYVDMIOETMKN 275

RESULT 2

QOYCN3 PRELIMINARY; PRT: 276 AA.

AC 09OYN3: 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hipostasin prostate type.
 GN PRSS20.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Yamaguchi N., Mitsui S.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Mitsui S., Mitsui S.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20525460; PubMed=11072088;
 RA Mitsui S., Okui A., Komihama K., Uemura H., Yamaguchi N.;
 RT "CDNA cloning and tissue-specific splicing variants of mouse
 hipostasin/TISP (PRSS20)."
 RL Biochim. Biophys. Acta 1494:206-210 (2000).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL: AB016227; BAA36955.1; -;
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.257; -;
 DR MGD: MGI:1929977; PRSS20.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPsin.
 DR SMART: SM0020; Tryp_SPC; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Protease; Serine protease.
 SQ SEQUENCE 276 AA; 30753 MW; 90BDC03A8AB178D6 CRC64;

Query Match 77.9%; Score 1187; DB 11; Length 276;
 Best Local Similarity 77.0%; Pred. No. 5, 2e-115;
 Matches 217; Conservative 28; Mismatches 31; Indels 6; Gaps 2;

QY 1 WQRLRLDWKSSGRGLTAKEPGARSSPLQAMRIQLILALATGLVGGETRIIKGPEC 60
 DB 1 MRLK--SDMKLS---TETREPARGAPALLQAMRIQLALALVGHVGGETRIIKGYEC 54
 QY 61 KHSQPMQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIYHLOQNLQKEGGEQRT 120
 DB 55 RHSPQWQVALFOKTRLLCGATLLAPRWLLTAHCKRPYVILLGEHMLEKTDGGEORRM 114
 QY 121 ATESPHPGPNNSLPKDKHRNDIMVYKASPVSIITAAVPLTLSSRCVATGSCISGMG 180
 DB 115 ATESPHPGPNNSLPKDKHRNDIMVYKASPVFTRAVOPLTLSPHCAVAGTSCISGMG 174
 QY 181 STSSPOLRLPHILRCANITIIIEHOKENAVPGNITDTWVCASVOEGKDCSGDSCGPIV 240
 DB 175 TTSSPOLRLPHILRCANVSIIEHKECEKAVPGNITDTWVCASVREKDCSGDSCGPIV 234
 QY 241 CNGSLQGIISWGODPCATRKPGVYTKVKYVDMIOETMKN 282

DB 235 CNGSLQGIISWGODPCATRKPGVYTKVKYVDMIOETMKN 276

RESULT 3

QOYCN4 PRELIMINARY; PRT: 249 AA.

AC 09OYN4: 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE HIPPOSTASIN (2310015108RIK protein).
 GN PRSS20 OR 2310015108RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Yamaguchi N., Mitsui S.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Mitsui S., Yamaguchi N.;
 RT "CDNA cloning of a novel brain serine protease, Hipostasin.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kanaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli V., Mommaerts P.,
 RA Noriote P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 DR EMBL: AB016226; BAA88825.1; -;
 DR EMBL: AK009720; BAB26461.1; -;
 DR EMBL: AK009360; BAB26241.1; -;
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.257; -;
 DR MGD: MGI:1929977; PRSS20.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00089; Trypsin; 1.
 DR SMART: SM0020; Tryp_SPC; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Protease; Serine protease.
 SQ SEQUENCE 249 AA; 27604 MW; P9F9CB457D727D5 CRC64;

Query Match 74.1%; Score 1123; DB 11; Length 249;
 Best Local Similarity 81.0%; Pred. No. 4, 9e-109;
 Matches 201; Conservative 24; Mismatches 23; Indels 0; Gaps 0;

QY 35 ILQILALATGLVGGETRIIKGPECRPHSPQWQVALFEKTRLLCGATLLAPRWLLTAH 94
 DB 2 ILRLIALALVGHVGGETRIIKGYECRPHSPQWQVALFOKTRLLCGATLLAPRWLLTAH 61

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QY 95 CLKPRYIVHLGOHNLQKEGCEOTRTATESFPHGFNNLSLPNKDHRNDIMLVKMASPVSI 154
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 CRPRHYIILGENHLEKTDGCBORRNATESFPHPDFNNLSLPNKDHRNDIMLVKMASSVFF 121

QY 155 TMAVRPLTLSSRCVTAAGTSCILISGWGSTSSPOLRLPHTLRCAANTIIIEHOCENAVPGNI 214
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 122 TRAVQPLTLSPHCVAAGTSCILISGWGSTSSPOLRLPHSLRCANVSIIEHECEKAYPGNI 181

QY 215 TDTMVCAVOEGGKDCSCGSGGGLVNCOSLOGIISWGDPICATRKPGYTYTVCKYVDW 274
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 182 TDTMLCASVRKEKDCSCGSGGGLVNCOSLOGIISWGDPICAVTRKPGYTYTVCKYFVW 241

QY 275 IOETMKNN 282
   |||:|||||:
DB 242 IHEVMKNN 249

RESULT 4
Q81W69 PRELIMINARY; PRT; 260 AA.
ID 081W69;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypoetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN 1)
RP SEQUENCE FROM N.A.
RC Straussberg R.;
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040887; AAI40887.1; -
KM Hypoetical protein.
SQ SEQUENCE 260 AA; 28090 MW; EF5934EB96295660 CRC64;

Query Match 45.4%; Score 692; DB 4; Length 260;
Best Local Similarity 49.2%; Pred. No. 1.4e-63;
Matches 125; Conservative 45; Mismatches 80; Indels 4; Gaps 3;

QY 26 RSSPLQAMRLQIL--ALATGLVGETRIIKGFCEKPHSOPMOALPEKTRLLCGATL 83
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 RPPRAKTMPLFLILGAWAGHSRAOEDKVLGHECQPHSOPWQALFQGGQLCGVL 62

QY 84 IABRWLLTAHCLKPRYIVHLGOHNLQKEGCEOTRTATESFPHGFNNLSLPNKDHRNDI 143
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 VGGNWTUTAHCKKPKYTVLGDHSLONKDPEDQIPVQSIHPHCYNSS-DVEDINHD 121

QY 144 MLVKMASPVSI TMAVRPLTLSSRCVTAAGTSCILISGWGSTSSPOLRLPHTLRCAANTIIIEH 203
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 122 MLQLDQSLGSKKRSISLADHCTQPGQKCTVSGMGTVSPRENPDPLNCAEVKIFQ 181

QY 204 OKENAYPGNITDTMVCAVOEGGKDCSCGSGGGLVNCOSLOGIISWGDPICATRKPG 253
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 182 KKCEDAVPGITVWVCAVSGSKA-DTCQDSSGGLVNCOSLOGIISWGSDDPCGRSDKPG 240

QY 264 VYTVCKYVDWIOE 277
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 VYTNICRYLDWIK 254

RESULT 5
Q96R00 PRELIMINARY; PRT; 255 AA.
ID 096R00;
AC 096R00;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Prostinogen.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN 1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21226193; PubMed=11327827;
RA Takayama T.K., Carter C.A., Deng T.;
RT "Activation of prostate-specific antigen precursor (pro-PSA) by
RT prostin, a novel human prostatic serine protease identified by
RT degenerate PCR.";
RL Biochemistry 40:1679-1687(2001).
CC EMBL; AF303046; AAK62813.1; -
DR HSSP; P00761; IAN1.
DR MEROPS; S01.081; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 255 AA; 27986 MW; 00D5B79E14B9468F CRC64;

Query Match 45.0%; Score 685.5; DB 4; Length 255;
Best Local Similarity 49.6%; Pred. No. 6.5e-63;
Matches 129; Conservative 40; Mismatches 76; Indels 15; Gaps 4;

QY 33 MRLQLILALATGLVGETRIIKGFCEKPHSOPMOALFEKTRLLCGATLAPRWLTA 92
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MWLLTLSPFLASTAQDGD-KLLEGECAHPQWPQVAYLERYGFRFGASLSPHWLVA 59

QY 93 AHCLKPRYIVHLGOHNLQKEGCEOTRTATESFPHGFNNLSLPNKDHRNDIMLVKMASPV 152
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 60 AHQSRFMRVRLGEHNLRRKDPEDQLRTTSRYIHPHRYE----ARSHRNDIMLRVOPA 115

QY 153 SITWAPRLTLSSRCVTAAGTSCILISGWGSTS-----SP--QLRPLTRCANITIE 202
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 116 RINPQVRPAVLPTRCHPEACVSGWGLVSHNEPCTAGSPSSQVSLPHTLRCAANTIGIS 175

QY 203 HOCENAYPGNITDTMVCAVOEGGKDCSCGSGGGLVNCOSLOGIISWGDPICATRKPG 262
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 176 DTSQDSYGRGLTNMTVCAVGAEGRAESCEGSGGLVCGILQGIIVSGNDVPCDNTTP 235

QY 263 GYTVCKYVDWIOETMKNN 282
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 236 GYTVCKYLEWIRETMKNN 255

RESULT 6
Q8CGR4 PRELIMINARY; PRT; 254 AA.
ID 08CGR4;
AC 08CGR4;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Prostin.
GN KLIK15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN 1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987;
RA Olsson A.Y., Lundvall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RT musculus.";
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN 12)
RP SEQUENCE FROM N.A.
RA Adame M., Mural R.;

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RU Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY152434; AAN78422.1; -
 SQ SEQUENCE 254 AA; 28042 MW; AA9E38BEDD01861 CRC64;

Query Match 44.9%; Score 683.5; DB 11; Length 254;
 Best Local Similarity 50.2%; Pred. No. 1e-62;
 Matches 128; Conservative 38; Mismatches 74; Indels 15; Gaps 4;

QY 36 LQILALATGLVGETRIIKGEFECKPHSQPMQALFEKTRLLCGATLIAPRWLLTAANC 95
 DB 3 LLLAFVLVSAADGD-KVLEGECEVPHSQPMQALFERGRFNCGAFLLSPRWLLTAANC 61
 QY 96 LKPRYIVHGOHNLQKEGCEQOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVST 155
 DB 62 QTRFKVRIRGEHNLRFDPGEQLRSVSRILPHPGYE---ARTHRDMLLRLFKPARLT 117
 QY 156 WVRPLTLSSRCVTAAGTSCGISGWC--STSSP-----QLRLPHTLRCANITIIHOK 205
 DB 118 AYVRPALPRRCPLIGEDCVSGKGLSDNNFGATGSKSHVRLPDLHCANISIISEAS 177
 QY 206 CENAYPGNITDTMVCASVQEGKSGQSGGPLYVCSGLGIIISWGDPCAITRKPGVY 265
 DB 178 CNKMDYPGRVLPMTMVCAGVEGGTDSCEGSDGGLVCGALQGVSWGDVPCDTTKPGVY 237
 QY 266 TVCKYVVDWIOETMK 280
 DB 238 TVCKYLEWIMENVR 252

RESULT 7

QY 08CGR6 PRELIMINARY; PRT; 276 AA.
 AC 08CGR6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Glandular kallikrein KLK13.
 GN KLK13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22325484; PubMed=12437987;
 RA Olsson A.Y., Lundwall A.;
 RT "Organization and evolution of the glandular kallikrein locus in Mus musculus."
 RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M., Mural R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY152432; AAN78420.1; -
 SQ SEQUENCE 276 AA; 30360 MW; 33E189C67492FDCA CRC64;

Query Match 44.5%; Score 678; DB 11; Length 276;
 Best Local Similarity 47.9%; Pred. No. 4.3e-62;
 Matches 127; Conservative 43; Mismatches 81; Indels 14; Gaps 3;

QY 29 PLQANRIIDLLILALATGLVGETRIK-----GFCECKPHSQPMQALFEKTRLL 77
 DB 3 PLVA--TIACTLTALASEGISRDYPKILNTNGTSGFLPGGYTCLPHSQPMQALLIRGL 60
 QY 78 LCGATLIAPRWLLTAANCILKPRYIVHGOHNLQKEGCEQOTRTATESFPHPGFNNSLPNK 137
 DB 61 LCGGVIVHVKWVLTAAHCKRDKGYTHLGHAGLRVENGQAMEVYRSTIHREYQVTPPHL 120
 QY 138 DHRNDIMLVKMASPVSTIWAVRPLTLSS-RCVTAAGTSCGISGSGTSSPQLRLPHTLRCA 196
 DB 121 RNDHDMLELKSPPVQLSSHVRLTKLSADDCLPYGCRCVSGWGTTSPQVNVYPTLQCA 180
 QY 197 NITIEHOKCENAYPGNITDTMVCASVQEGKSGQSGDGGPLVCSGLIISWGDPCC 256

DB 161 NIELSDECEQVYPGKITANMLCAGTKEGKSGCSDGSGPLICNGKLYGIIISWGDPCC 240
 QY 257 AITRKPGVYTVCKYVVDWIOETMKX 281
 DB 241 GQNRPGYTRVSKYLRWIRRIIN 265

RESULT 8

QY 09DBO8 PRELIMINARY; PRT; 251 AA.
 AC 09DBO8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE 1200016C12Rik protein.
 GN 1200016C12Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.W., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereis P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL: AK004807; BAB23579.1; -
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.307; -
 DR MGD: MGI:1921082; 1200016C12Rik.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR SMART: SMO0020; Tryp_Spc; 1.
 DR PROSITE: PSS0240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR HydroLase: Protease; Serine protease.
 SQ SEQUENCE 251 AA; 28153 MW; FAD667F8C80C4A23 CRC64;

Query Match 43.7%; Score 665; DB 11; Length 251;
 Best Local Similarity 51.0%; Pred. No. 8.7e-61;
 Matches 126; Conservative 40; Mismatches 81; Indels 0; Gaps 0;

QY 36 LQILALATGLVGETRIIKGEFECKPHSQPMQALFEKTRLLCGATLIAPRWLLTAANC 95
 DB 5 LTVVLFSLAACHGADTRAVARGCVNSXWQAGFLYLRQLCGATLIINQWLLTAHC 64
 QY 96 LKPRYIVHGOHNLQKEGCEQOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVST 155
 DB 65 RKPVLWVRLGHHLMRWEGPQLLVTDFEPHPPFNPLSANDHNDMLIRLPKRVLT 124
 QY 156 WVRPLTLSSRCVTAAGTSCGISGSGTSSPQLRLPHTLRCANITIIHOKCENAYPGNIT 215

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Db 125 PAQPLNLTESRPVPVOTQCLIFGMGVSSSKLOYPMTLQCANISIIDNKCFWAYPGHIF 184
QY 216 DTIVCAVOEGKDSGCGSGGPLVNCNOSLOGIISMGODPCATRKRGVYTKCKVDM 275
Db 185 KKLICAGLWEGSGSCGCGDFGFLVCEGTLAGIVFGFEGPCSRPRPVAITVFDYLEWI 244
QY 276 QETMKNN 282
Db 245 ESPMEKN 251

RESULT 9
Q9D140 PRELIMINARY; PRT; 293 AA.
AC Q9D140;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
GN 1110030019R1K protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata S.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasikawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuenli P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guelincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Williams L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashiaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AK003966; BAB23113.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.017; -.
DR MEROPS; S01.418; -.
DR MGD; MG1:1915918; 1110030019R1K.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser protease_Try.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Hydrolase; Protease; Serine protease.
SQ SEQUENCE 293 AA; 31908 MW; ED1F45D8226FE911 CRC64;

Query Match 41.5%; Score 632; DB 11; Length 293;
Best Local Similarity 45.8%; Pred. No. 2,8e-57;
Matches 114; Conservative 49; Mismatches 72; Indels 14; Gaps 5;
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QY 95 CLKPRYIVHAGHNLQK-EEGCEQRTATESFPHPGNSLPNKHNDIMLVKASPV 153
Db 110 CKRPVRIIRLGHNSMSPVYESQGMFGKSLPHPEVS----HFGSNLMLIKMKRK 165
QY 154 ITWAVRPLTLSSRCVTAGTSCILSGWGSTSSPOLRLPHLRNCANITIEHQENAPGN 213
Db 166 DSHSVKPEIACDCATEGTRCMVSGWGTSSSHNNPFLVQCLINTVLSEERCKNSPQ 225
QY 214 ITDTWVCASVOEGKDSGCGSGGPLVNCNOSLOGIISMGODPCATRKRGVYTKCKYVD 273
Db 226 IOKTFECADDEB-GRDSCGDSGFPVNCGLQGLVSWDFPCQQRNRPBGVYTNLCEFYK 284
QY 274 WIOETMKNN 282
Db 285 WIKDTMNSN 293

RESULT 10
Q8CGR5 PRELIMINARY; PRT; 250 AA.
AC Q8CGR5;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Glandular kallikrein KLK14.
GN KLK14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987;
RA Olsson A.Y., Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RT musculus.";
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY152433; AAN78421.1; -.
SQ SEQUENCE 250 AA; 27016 MW; F62FEBF2290FBB8 CRC64;

Query Match 41.1%; Score 626; DB 11; Length 250;
Best Local Similarity 46.1%; Pred. No. 9,8e-57;
Matches 117; Conservative 43; Mismatches 86; Indels 8; Gaps 3;
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QY 33 MRLQILILATATGLV--GGERRIIKGFECRPHSQPQALFEKT--RLTGGATLIAPRW 88
Db 1 MFLDILIIQALVAIAQSGQGDHKLITGYRCVANSQPMVOVALAGGHRFLCGVLLSDQW 60
QY 89 LTTAAHCLKPRYIVHAGHNLQK-EEGCEQRTATESFPHPGNSLPNKHNDIMLVK 148
Db 61 VITAHCARPIILHVALGHNIRMEATQGVAVARQVHPQVQ----FGAHNDMLKL 116
QY 149 ASPVSTIWAVRPLTLSSRCVTAGTSCILSGWGSTSSPOLRLPHLRNCANITIEHQECN 208
Db 117 QKRVLRGRAVVTISVASSCASPGTRCVSGMTIASPIARVPTALQCVVNIINSQACHR 176
QY 209 AVPGVITDTWVCASVOEGKDSGCGSGGPLVNCNOSLOGIISMGODPCATRKRGVYTKV 268
Db 177 AVPGIITGMCVACAGPEBGKDSGCGSGGPLVCGQLGLVSWGMRCAKPGVPGVYANL 236
QY 269 CKYVDWIOETMKNN 282
Db 237 CNVHSWIKRTWQSN 250

RESULT 11
Q9JW70 PRELIMINARY; PRT; 261 AA.
```

AC 09JW70;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Glandular kallikrein 21 (Similar to kallikrein 21).
 GN KLK21 OR GK21.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20534760; PubMed=11082197;
 RA Matsui H., Moriyama A., Takahashi T.;
 RT "Cloning and characterization of mouse Klk27, a novel tissue
 kallikrein expressed in testicular Leydig cells and exhibiting
 RT chymotrypsin-like specificity";
 RT Eur. J. Biochem. 267:6858-6865(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Salivary gland;
 RA Strausberg R.;
 RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB039276; BAA92319.1; -;
 DR EMBL; BC012243; AAI12243.1; -;
 DR HSSP; P00757; ISGF.
 DR MEROPS; S01.038; -;
 DR MGD; MGI:892022; Klk21.
 DR InterPro; IPR001254; Ser.protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Protease; Serine protease.
 SQ SEQUENCE 261 AA; 28690 MW; 608B976BC78E03EE CRC64;

Query Match 39.5%; Score 602; DB 11; Length 261;
 Best Local Similarity 42.5%; Pred. No. 3.2e-54;

Matches 111; Conservative 51; Mismatches 87; Indels 12; Gaps 3;

QY 33 MFIQLLILALATGIVG---ETRIKFECKPHSQPWQAALFEKTRLLCGATLIAPRW 88
 DB 1 MFLL-ILFLALSLGEIDAAPVQSRIVGFCNCKSQSPWHAVALFRNKYICGCVLNPW 59
 QY 89 LITAAHCLKPRYIVHLGQNLQKEGCEQRTATATESFPHPGFNNSL-----PNKDHKN 141
 DB 60 VLTAAHCVGNQYVNLGKKNKLFQHESSAQHRLVSKSFPHPDVNMGLMDHTPHREDVSN 119
 QY 142 DIMLVKASPVSIITWAVRPDLTSSRCVTAGTSCLSGWSSTSSPOLRLPHLTRCANITII 201
 DB 120 DLMRLRSKPADITPAVKPIDPTEPRKLGSTCLASGWSITPTKWOIIPNDLQCGFIRPL 179
 QY 202 EHOKENAVPGNITPTMVCASVOEGKDSQCGDSGGLVNCNLSGGIISWGDPCAIRK 261
 DB 180 PNEACAIAIHKVTDVMLCAGEMGGKDTCADSGSGLICDVGITISWGSIPCAKPNA 239
 QY 262 PGVYTKVCKYVDMIQETMKN 282
 DB 240 PAIYTKLIKFTSMIKDTMAKN 260
 RESULT 12
 Q9ZIR9 PRELIMINARY; PRT; 246 AA.
 AC Q9ZIR9;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE TRYPSINogen 16.
 GN TRYCN16 OR TRYPSINOGEN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/c;
 RA Rowen L., Hood L.;
 RT "Comparison between strains Balb/c and 129 in a region of the mouse T
 cell receptor beta locus."
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Balb/c;
 RA Chen F., Rowen L., Hood L., Rothenberg E.V.;
 RT "Differential transcriptional regulation of individual TCR Vbeta
 segments before gene rearrangement";
 RL J. Immunol. 166:1771-1780(2001).
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AF107342; AAC79093.1; -;
 DR EMBL; AE000665; AAB69088.1; -;
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.063; -;
 DR MGD; MGI:2148749; Trypnl6.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser.protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Protease; Serine protease.
 SQ SEQUENCE 246 AA; 26134 MW; 34E173B18CA2FA63 CRC64;

Query Match 39.4%; Score 600.5; DB 11; Length 246;
 Best Local Similarity 47.4%; Pred. No. 4.3e-54;

Matches 120; Conservative 38; Mismatches 88; Indels 7; Gaps 4;

QY 30 LQAMRIQLILALATGIVGETRIKFECKPHSQPWQAALFEKTRLLCGATLIAPRW 89
 DB 1 MSALLFLVGAQAAVFP-VDDDDKIVGGYTCRENSVPAQVSL-NSGYHFCGSLINDQMV 58
 QY 90 LTAHCLKPRYIVHLGQNLQKEGCEQRTATATESFPHPGFNNSLPPNDHNDIMLVGMA 149
 DB 59 VSAHCYTRIQVRLGHEHNVLEGNEDFIDPAKIKIPNPKRTLN---NDIMLILKS 114
 QY 150 SPVSIITWAVRPDLTSSRCVTAGTSCLSGWSSTSSPOLRLPHLTRCANITIIEHOKENA 209
 DB 115 SPVTLNARVALPSSCAPAGTQCLISGWKNTISFGVSEEDLQCIDAPLPPQADCEAS 174
 QY 210 YPGNITDTMVCASVOEGKDSQCGDSGGLVNCNLSGGIISWGDPCAIRKPGVYTKVC 269
 DB 175 YPGKITGNMVCAGFLEGKDSQCGDSGGLVNCNLSGGIISWGYG-CALPNNPGVYTKVC 233
 QY 270 KYVDMIQETMKN 282
 DB 234 NYVDMIQETIAAN 246
 RESULT 13
 Q9CV76 PRELIMINARY; PRT; 234 AA.
 AC Q9CV76;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE 2310008B01RIK protein (fragment).
 GN 2310008B01RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AK009217; BAB26143.1; -;
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.020; -;
 DR MGD; MGI:1916761; 2310008B01Rik.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Protease; Serine protease.
 KW NON TER
 FT 1
 SQ SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;
 Query Match 39.4%; Score 599.5; DB 11; Length 234;
 Best Local Similarity 46.8%; Pred. No. 5.1e-54;
 Matches 108; Conservative 40; Mismatches 78; Indels 5; Gaps 4;
 QY 53 RIHKGECKPHSQPQALPEKTRLLCGATLLAPRWLLTAHCKRYIVHGOHLQKE 112
 DB 8 KLYNGVECVKNSQPVGVGFHCKRYLGGVLDVRKWLTAHCRDKYVVRGESHSLTL 66
 QY 113 EGCEQRTATSEFPHPGFNNSLPNKDHRDMLVKMASPVSIITWAVRPLTLSSRCVTAGT 172
 DB 67 DWTEQURHTFTSTHSYQAYON--HEHDLRLRLNRPIHLTRAVRPALSSCVTTGA 124
 QY 173 SCLISGWSGTSFQFLPHTLRCANITIEHOKCENAYGNTITWVCASVOEGKDSQ 232
 DB 125 MCHVSGMGTNNKMPDPRLQCLNISTVSNETCRVFGRAVENMLCAG-GEAGKDAQ 183
 QY 233 GDSGGLVGNQSLGGIISWGQ--DPCALTRKPGYTVCKYVVMIOGTMMKN 282
 DB 184 GDSGGLVGVVLGGVLGSLVSGVPGCGKGIPIGVYTKVCKYTDWIRIVRNN 234

RESULT 14
 OSROT7 PRELIMINARY; PRT; 246 AA.
 AC OSROT7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE Pancreatic trypsin (0910001B19RIK protein) (Trypsinogen 8).
 GN TD OR 0910001B19RIK OR TRYPSINOGEN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SVJ;
 RX MEDLINE=99436155; PubMed=10506205;
 RA Ohmura K., Kohno N., Kobayashi Y., Yamagata K., Sato S.,
 RA Kashiwabara S., Baba T.;
 RT "A homologue of pancreatic trypsin is localized in the acrosome of
 RT mammalian sperm and is released during acrosome reaction";
 RL J. Biol. Chem. 274:29426-29432(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Stomach, and Spleen;
 MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=21103195; PubMed=11160223;
 RA Chen F., Rowen L., Hood L., Rothenberg E.V.;
 RT "Differential transcriptional regulation of individual TCR Vbeta
 RT segments before gene rearrangement";
 RL J. Immunol. 166:1771-1780(2001).
 CC -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AB017032; BAA74761.1; -;
 DR EMBL; AK008667; BAB25821.1; -;
 DR EMBL; AK003064; BAB25242.1; -;
 DR EMBL; AE000664; AAB69056.1; -;
 DR HSSP; P00763; ISLU.
 DR MEROPS; S01.057; -;
 DR MGD; MGI:1913350; 0910001B19RIK.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Protease; Serine protease.
 KW NON TER
 FT 1
 SQ SEQUENCE 246 AA; 26274 MW; B6A9FAC99079633F CRC64;
 Query Match 39.3%; Score 598.5; DB 11; Length 246;
 Best Local Similarity 46.6%; Pred. No. 6.9e-54;
 Matches 118; Conservative 41; Mismatches 87; Indels 7; Gaps 4;
 QY 30 LQAMRIQLILALATGVLGSETRIKGECKPHSQPQALPEKTRLLCGATLLAPRWL 89
 DB 1 MRALFLVLAAGAAVFP-VDDDKLVGGYTCRENSVPQVSL-NSGYHFCGSLINDQV 58
 QY 90 LTAHCLKPRYIVHGOHLQKEGCEQRTATSEFPHPGFNNSLPNKDHRDMLVKMA 149
 DB 59 VSAHCVKRSIROVRGHNINVLGEGNEQFVNSAKIKHPNNSRTL---NDIMLIKLA 114

QY 150 SPVSTTAVRPLTLSSRCVTAGTSCISGWSSTSPQLRPLPTRLRCANITIEHOKCENA 209
DB 115 SPVTLNARVATVAPLSSCAPAGTQCLISGWNLTSLFGVNNPDULQCLDAPLPLQADCEAS 174
QY 210 YGNTITDPMVCASVQEGKSCGDSGGPLVGNOSLOGIISWGDPICATRKRGVYTKVC 269
DB 175 YPGKITNNHCYGFLEGGKSCGDSGGPVCNGOLQIVSWGYC-CALKDNPVYITKVC 233
QY 270 KYVDWIQETMKN 282
DB 234 NYVDWIQNTIAAN 246

RESULT 15

Q63275 PRELIMINARY; PRT; 239 AA.
ID Q63275
AC Q63275;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Kallikrein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Submandibular gland;
RA Zintz C.B., Ma J.-X., Chao J., Chao L.;
RT "Isolation and characterization of a new rat kallikrein cDNA with
predominant expression in the kidney."
RL Submitted (JAN-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; U33840; AAA58782.1; -.
DR HSSP; P00759; 1TON.
DR InterPro; IPR001254; Ser_protease_Try.
DR pfam; PF00089; trypsin; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Protease; Serine protease.
FT NON_TER
SQ SEQUENCE 239 AA; 26382 MW; 3CBD761AF06ABB53 CRC64;

Query Match 39.2%; Score 597.5; DB 11; Length 239;
Best Local Similarity 44.8%; Pred. No. 8.5e-54;
Matches 107; Conservative 48; Mismatches 73; Indels 11; Gaps 3;

QY 50 GETRIIKGPECKPHSQPMQALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQNTL 109
DB 5 GQSRVVGGRCKEKNQPMQVAVINED--LCGGVLIDPSVITPAHCYSDNYHVLGGNNL 62
QY 110 QKEEGCEOTRTATESPPHPGF-----NNSLPKDHNDIMLVKMASPVSIWAVRPLTL 163
DB 63 SED---VQHRVLVSQSRPHPDYKPLMKNTTRKPKDYSDNLMHLHSEPADITDGKVIDL 119
QY 164 SSRCTAGTSCISGWSSTSPQLRPLPTRLRCANITIEHOKCENAYPGNITDTWVCASV 223
DB 120 PTKRPVSGTCLVSGWGTNPSEMEFPDDLQCVNIHLNNEKCIKAYKEKVTDLMLCAGE 179
QY 224 QEGGKDSGCGDSGGPLVGNOSLOGIISWGDPICATRKRGVYTKVCYVDWIQETMKN 282
DB 180 LEGGKDTCRGDSGGPLICDGLQGITWSGVPCEPNKPGIYTKLIKFTSWIKEVWKKN 238

Search completed: October 22, 2003, 15:53:09
Job time : 37.319 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 15:36:10 ; Search time 2423.21 Seconds
(without alignments)
2828.419 Million cell updates/sec

Title: US-09-856-320A-2
Perfect score: 1523
Sequence: 1 MQRRLRWLRDMKSSGRGLTAA.....GYVTKVCKYVDWIQETMKUN 282

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame-p2n.model -DRV=xlh
-Q=/cgn2_1/USPTO.spool/US09856320/runat_22102003_121415_25672/app_query.fasta_1.846
-DB=EST -QFMT=fastap -SUFPIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blonum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pcst -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=PCO -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09856320.@CCN_1_1_3596.@runat_22102003_121415_25672 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: em_estba:*
2: em_estchum:*
3: em_estcin:*
4: em_estcnu:*
5: em_estcov:*
6: em_estcpl:*
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8: em_htc:*
9: gb_estc1:*
10: gb_estc2:*
11: gb_htc:*
12: gb_estc3:*
13: gb_estc4:*
14: gb_estc5:*
15: em_estcom:*
16: em_estfun:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_pod:*
26: em_gss_tod:*
27: em_gss_vr1:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1488.5	97.7	1294	11	BC015551 Homo sapi
2	1377.5	90.4	1072	12	BM559782 AGENCOURT
3	1326.5	87.1	1074	12	BM559617 AGENCOURT
4	1284	85.0	853	10	BG720793 602692015
5	1187	77.9	1295	11	AK009360 Mus muscu
6	1187	77.9	1295	11	AK009720 Mus muscu
7	1161	76.2	1269	11	AK009659 Mus muscu
8	1158	76.0	841	12	B1818697 603037514
9	1146	75.2	678	12	B1763040 603047836
10	1110	72.9	708	10	BG697071 602660281
11	1021	67.0	973	10	BE867930 601443517
12	975	64.0	639	10	BG747134 602704354
13	816	53.6	539	12	BM837078 K-EST0113
14	794	52.1	579	12	B1046611 MR3-FN020
15	780	51.2	761	12	BM982377 UI-CF-EN1
16	775	50.9	528	4	BX528424 RZPD Mus
17	744.5	48.9	747	13	BX109836 BX109836
18	724	47.5	967	9	A1893370 mJ99H09.Y
19	723.5	47.5	966	14	BY709314 BY709314
20	720	47.3	467	9	AA073833 mJ99H09.X
21	692.5	45.5	898	14	CB204935 AGENCOURT
22	690.5	45.3	880	14	CB202840 AGENCOURT
23	687	45.1	526	10	BE898804 601681783
24	685	45.0	809	10	BF679282 602153475
25	678.5	44.6	852	14	CB587168 AGENCOURT
26	669	43.9	1048	11	AK004807 Mus muscu
27	653.5	42.9	826	14	CB574882 AGENCOURT
28	640	42.0	484	14	CB270157 Mus muscu
29	632	41.5	1240	11	AK003996 Mus muscu
30	626	40.7	673	13	BU684799 UI-CF-EN1
31	620.5	40.1	368	9	AA412318 zt97606.X
32	617	40.5	754	12	B1653899 603280742
33	613	40.2	765	13	BX079152 BX079152
34	613	40.2	766	13	BU416879 603670939
35	613	40.2	808	13	BU416510 603670980
36	613	40.2	857	13	EX078781 BX078781
37	612	40.2	834	13	BU487089 603972168
38	610	40.1	750	13	BU492376 604130628
39	610	40.1	783	13	BU417086 603671080
40	610	40.1	786	13	BU417396 603670539
41	610	40.1	800	13	BU417373 603671011
42	610	40.1	806	13	BU416343 603671007
43	610	40.1	816	13	BU417211 603671638
44	609	40.0	742	13	BU417425 603670892
45	609	40.0	811	13	BU417330 603671691

ALIGNMENTS

RESULT 1
LOCUS BC015551 1294 bp mRNA linear HTC 29-OCT-2001
DEFINITION Homo sapiens, kallikrein 11, clone IMAGE:3847565, mRNA.
ACCESSION BC015551
VERSION BC015551.1 GI:15930236
KEYWORDS HTC
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1294)
AUTHORS Strausberg,R.

TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LNL)
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdbaxil@stanford.edu
 R. M.
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R.

FEATURES
 source
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAX Plate: 20 Row: 1 Column: 12
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gt: 8574438
 This clone has the following problem: frame shifted.
 location/Qualifiers
 1. 1294
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="locusID:11012"
 /db_xref="taxon:9606"
 /clone="IMAGE:3847565"
 /tissue_type="Colon, adenocarcinoma"
 /clone_id="NH_MGC_65"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
 BASE COUNT 317 a 391 c 334 g 252 t
 ORIGIN

Alignment Scores:
 Pred. NO.: 2,75e-127 Length: 1294
 Score: 1488.50 Matches: 281
 Percent Similarity: 99.30% Conservative: 1
 Best Local Similarity: 98.94% Mismatch: 0
 Query Match: 97.73% Indels: 2
 DB: 11 Gaps: 1

US-09-856-320A-2 (1-282) x BC015551 (1-1294)

QY 1 MetGlnArgLeuAgtTgTpleuArgAspTryLysSerSerGlyAArgGlyLeuThAlaAla 20
 Db 119 ATGAGAGAGTTGAGAGTGGCTGCGGAGACTGGAAGTCATCGGGCAGAGGCTTCACAGCAGCC 178

QY 21 LysGlnProGlyAlaArgSerSerProLeuAlaMetArgIleLeuGlnLeuIleu 40
 Db 179 AAGGAACCTGGGGCCCGCTCTCCGCCCTCCAGGCCATGAGATTTCGACTTAATCTGT 238

QY 41 LeuAlaLeuAlaThrgIlyLeuValGlyGlyGlnThrArgIleIleLysGlyPheGluCys 60
 Db 239 CTTGCTGTGGCAACAGGGCTTGTAAGGGGAGACACAGATCATCAAGGGGTTGAGATGC 298

QY 61 LysProHisSerGlnProTgTgAlaAlaLeuPheGluLysThrArgLeuLeuCysGly 80
 Db 299 AAGGCTCACTCCAGCCCTGGCAGAGCCCTGTTCNAAGAGCGGCTTACTGTGGG 358

QY 81 AlaThrLeuIleAlaProArgTgTpleuLeuThraAlaHisCysLeuLysPro----Ar 99
 Db 359 GCGAGGCTCATGCCCCCAGATGGCTCTGACACAGAGCCACTGCTCAAGCCCTGGCCG 418

QY 99 GTTCTTLeuAlaHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrAr 119
 Db 419 CTACATGATTCACCTGGGGCAGCACCAACTCCAAAGAGAGGAGGCTGTAGACGACGCCG 478

QY 119 gTThAlaThrcIuSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHi 139

Dn		479	GACAGCGCATGAGTCTTCCTCCCAACC	GGCGGTTCACACAGCCTCCCAACAAGGCCA	538
Oy		139	sarpsanaasp1 ewetlevalys mevalas serprovalser1 ethrtpalava ar		159
Dn		539	CCGCATGACATCATGCTGTGAAGATGGCATCCGCAGTCTCCATCACCTGGCGTGCG		598
Oy		159	gproleuthrlenserserArCyValThAlAglyThrserylsenuleserglyTr		179
Dn		599	ACCCCTCACCCCTCTCTCACGCTGTGTACTGTGGACACACAGCTGCTCATTTCCGGCTG		658
Oy		179	pGlySerThrserSerProglInLeuArgLeuProH;SthrleuArgCysAlaasn1 eth		199
Dn		659	GGGACGACAGCTCCAGCCCCCACTTAGCGCTCTCCACACCTTGGATGCCCAACATCAC		718
Oy		199	r1 elieglnHsglnYscYsgluAsna1 Ty-ProGlyAsn1 eThrasPthrxv		219
Dn		719	CATCATTTGAGCACAGAAAGTGTGAGAAGCCTTACCCCGGCAATCACACACATGCT		778
Oy		219	lcyalsalaservAlnglnglyglylyVaspservCysGlnglyVaspservglyVole		239
Dn		779	GGTGCGCACCGCGACGAAAGGGGGGCAAGACTCTCTCGACAGGTGACTCCGGGGCCCTCT		838
Oy		239	vualCysAsngInsarsleauglnglylle1 setrTgIyGlnaspProcysAla1 eth		259
Dn		839	GGTGTGTAAACAGCTCTCTTCAAAGCATTAATCTCTGGGGCCAGATCCGTGTGCGATCAC		898
Oy		259	rArgLysProglYvalTYrThrvLyvalCysLYsTYr-Va1aspTp1 eglngluThrxw		279
Dn		899	CCGAAAGCTGGTGTCTACAGAAAGTCTGCAATATGTGGACTGATTCAGAGACAGAT		958
Oy		279	tlysAsnaen	282	
Dn		959	GAAGAACAT	968	
RESULT 2					
LOCUS	BMS59782		1072 bp	mRNA	linear EST 20-FEB-2000
DEFINITION	AGENCOURT_6565460 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:574441				
ACCESSION	BMS59782				
VERSION	BMS59782.1 GI:18803655				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleosomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.				
TITLE	NIH-MGC http://mgs.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: csgrabs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LLM12765 row: 1 column: 11 High quality sequence stop: 684. Location/Qualifiers 1..1072 /organism="Homo saplens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5744410" /tissue_type="medulla" /lab_host="DH10B" /clone_id="NIH_MGC_119" /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NciI; Site_2: EcoRV (destroyed); RNA source normal medulla from				
FEATURES					
source					

anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

BASE COUNT 238 a 340 c 307 g 185 t 2 others

ALIGNMENT SCORES:

Pred. No.: 3.9e-117 Length: 1072
Score: 1377.50 Matches: 265
Percent Similarity: 96.39% Conservative: 2
Best Local Similarity: 95.67% Mismatches: 7
Query Match: 90.45% Indels: 3
DB: 12 Gaps: 1

US-09-856-320A-2 (1-282) x BM559782 (1-1072)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyValArgGlyLeuThrAlaAla 20
DB 116 ATGAGAGGTTGAGGTGGCTGGGAGCTGGAAGTCAGGCGAGAGTCTCAGACAGACC 175
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
DB 176 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCCATGAGATTCTGCGATTATCTCTG 235
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGluCys 60
DB 236 CTTCCTCTGGCAACAGGGCTTGTAGGGGGAGAACACAGGATCATCAAGGGGTTGAGTGC 295
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
DB 296 AACCTCATCTCCAGCCCTGGCAGGAGCCCTTTGAGAAAGCGGGCTACTCTTGGG 355
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 356 GCGAGCTCATGCGCCCGAGATGGCTCCGACAGCAGCCAGCTGCTCAAGCCCGCTAC 415
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGluGlnThrArgTyr 120
DB 416 ATGTGTACCTGGGGAGCACAACCTCCAGAAAGAGAGGGCTGTGACAGACCCGAGACA 475
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 476 GCCACTGAGCTCTTCCCGACCCCGGCTTCAACAGCGCTCCCGCAACAAAGCCACGCC 535
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 536 AATGACATCATGCTGTGTAAGATGAGATGCCATGCCAGTCTCCATCACTGNGCTGTGCAACC 595
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
DB 596 CTCACCTCTCCCTCAAGCTGTGCTGCTGAGGACAGCAGCTGCTATTTCCGGCTGGGG 655
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 656 AGCAGCTCAGCCCGCAGTTAGCCTGCTCAGCCTTCCAGTCCCGCAACATCACCATC 715
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
DB 716 ATTGAGCACAAGAGTGTAGAAAGCGCTTACCCCGGCAATCAGACACCATGTGTGT 775
QY 221 AlaSerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
DB 776 GCCAGGCTCAGAGAGGGGCAAGGAGCTCTGNCAGTGACTCCGGGGCCCTCGATC 835
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGly-GlnAspProCysAlaIleThrArg 260
DB 836 TGTAAACAGCTCTTTAAGGCATTATCTCTGGGGGAGAGATCCGTGTGCATACCCG 895
QY 260 glyspGlyValTyrThr---LysValCysLysTyrVal-AspTrp 274

DB 896 GAAAGCTGTGTCTACCCGAAAGGTCGCAATATGTGGAGCTGG 942

RESULT 3
LOCUS BM559617
DEFINITION BM559617 1074 bp mRNA linear EST 20-FEB-2002
AGENCOURT 6565456 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5744314
5', mRNA sequence.
ACCESSION BM559617
VERSION BM559617.1 GI:18803348
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1074)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-rc@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM12765 row: h column: 11
High quality sequence stop: 689.
Location/Qualifiers
1. 1074
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/mol_type="mRNA"
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/clone="IMAGE:5744314"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_lib="NIH_MGC_119"
/note="Organ: Brain; Vector: pCMV-SPORT6; Site: 1. NCI;
Site: 2. EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH MGC Library."

FEATURES

source

Alignment Scores:
Pred. No.: 2.06e-112 Length: 1074
Score: 1326.50 Matches: 265
Percent Similarity: 93.71% Conservative: 3
Best Local Similarity: 92.66% Mismatches: 12
Query Match: 87.10% Indels: 6
DB: 12 Gaps: 1

US-09-856-320A-2 (1-282) x BM559617 (1-1074)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyValArgGlyLeuThrAlaAla 20
DB 115 ATGAGAGGTTGAGGTGGCTGGGAGCTGGAAGTATCGGGAGAGTCTCAGACAGACC 174
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
DB 175 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCCATGAGATTCTGCGATTATCTCTG 234
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGluCys 60
DB 235 CTTCCTCTGGCAACAGGGCTTGTAGGGGGAGAGAACACAGATCATCAAGGGGTTGAGTGC 294

QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
 Db 295 AAGCCCTCCTCCAGCCCTGGAGGAGGAGCCCTGTTGAAAGACGGGCTACTCTGTGG 354
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 Db 355 GCGAGCCTCATGCCGCCAGATGGCTCTCGACAGAGCCACTGCTCAAGCCCGCTAC 414
 QY 101 IleValHisLeuGlnGlnHisAsnLeuGlnLysGlnGlnCysGlnGlnThrArgThr 120
 Db 415 ATAGTTACCTGGGGAGAGCAACCTCCAGAGAGAGAGGCTGTGACAGACCCGAGACA 474
 QY 121 AlaThrGlnSerPheProHisProGlnPheAsnAsnSerLeuProAsnLysAspHisArg 140
 Db 475 GGCACGTAGTCTTCCGCCACCCCGGCTTCACAAAGAGGCTCCCAACAAAGACACCGC 534
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 Db 535 AATGACATCATGCTGTGTAAGATGGCATGCCATGCTCCATCATCACTGGGCTGTGACACC 594
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
 Db 595 CTCACCTCTCTCCAGCTGTGTGCTGCTGGAGCAGCTGCTCATTTCCGGCTGGGGC 654
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 Db 655 AACACGCTCAGGCCCCAGTTAGCCCTGCTCACACCTTCGATGGCCCAACATCACACATC 714
 QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlnAsnIleThrAspThrMetValCys 220
 Db 715 ATTGAGCACCAAGATGTAGAAAGCCCTTACCCGGGCAATACACAGACCCATGTGTGT 774
 QY 221 AlaSerValGlnGlnGlnGlyLysAspSerCysGlnGlnLysAspSerGlyGlyProLeuVal 240
 Db 775 GCGAGCGTCAGAGAGGGGAGGAGGAGCTCTGTCAGAGGAGTACCTCGGGGGGCTCTGTGT 834
 QY 240 LysAsnGlnSerLeuGlnGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThr 259
 Db 835 CTGGTACCAAGTCTTCAAGGATTAATCTCTGGGGGAGCAAGATCCGTGTGTCGATCAC 894
 QY 260 ArgLysProGlnValTyrThrLysValCysLysTyrVal---AspTrpIleGlnGlnT 278
 Db 895 CCAAAAGCCTGTGGTACCCCAAAAGTCTTGCAATATGTGGACTGATCCCGGAGACA 954
 QY 278 hMetLys 280
 Db 955 CCATGGAG 962
 RESULT 4
 BG720793 853 bp mRNA linear EST 08-MAY-2001
 LOCUS 60269201SF1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4824387 5',
 DEFINITION mRNA sequence.
 ACCESSION BG720793
 VERSION BG720793.1 GI:13999980
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 853)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-rt@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
 Toshitaki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LLM10735 Row: n Column: 04
 High quality sequence stop: 826.
 Location/Qualifiers
 1..853
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4824387"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 97"
 /note="Organ: testis; Vector: pBluescriptPR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (cgccgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.2 kb and normalized to 10^5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
 BASE COUNT 180 a 285 c 227 g 161 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,48e-109 Length: 853
 Score: 1294.00 Matches: 248
 Percent Similarity: 98.42% Conservative: 1
 Best Local Similarity: 98.02% Mismatches: 3
 Query Match: 84.96% Indels: 2
 DB: 10 Gaps: 0
 US-09-856-320a-2 (1-282) x BG720793 (1-953)
 QY 21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
 Db 97 GAGGAGCTGGGGCCGCTCTCTCCCTCAGGCAATGAGATTCGCAATTAATCTG 156
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyThrArgIleIleLysGlyPheGlnCys 60
 Db 157 CTTCCTCTGGCAAGAGGCTGTGTGAGGGGAGAGACAGATCATCAAGAGGCTGAGTGC 216
 QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
 Db 217 AAGCTCATCTCCAGCCCTGGAGAGAGCCCTGTTCCAGAGAGCGGCTACTCTGTGG 276
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 Db 277 GCGAGCCTCATGCCGCCAGATGGCTCTCGACAGAGCCCACTGCTCAAGCCCGCTAC 336
 QY 101 IleValHisLeuGlnGlnHisAsnLeuGlnLysGlnGlnCysGlnGlnThrArgThr 120
 Db 337 ATAGTTACCTGGGGAGAGCAACCTCCAGAGAGAGGAGGCTGTGAGCAGACCCGAGCA 396
 QY 121 AlaThrGlnSerPheProHisProGlnPheAsnAsnSerLeuProAsnLysAspHisArg 140
 Db 397 GCCACTGATCTTCTCCCAAGCCCGGCTTCAACAACAGCTCCCAACAAAGACACCGC 456
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 Db 457 AATGACATCATGCTGTGTAAGATGGCATGCCATCTTCATCACTGGGCTGTGACACC 516
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
 Db 517 CTCACCTCTCTCCAGCTGTGTACAGCTGGCACAGCTGCTCATTTCCGGCTGGGGC 576
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 Db 577 AGCAGCTCAGCCGCCAGTTAGGCTGCTCACACCTTGCGATGGCCCAACATCACATC 636
 QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlnAsnIleThrAspThrMetValCys 220
 Db 637 ATTGAGCACCAAGATGTAGAAAGCCCTTACCCGGGCAACATCAAGACACCATGTGTGT 696

Oy	221	laasrVal1gIngluG1yVlyksapsrCysgIngluYaspserC1y1ProleuVal	240
Db	637	GCACCGTCACGAGGAGGAGGACAGGACTTCCTCCAGTT-GACTCCGGGGCCCTTGTC	755
Oy	241	-CysanGlnserLeuGIngluY1le1seerTrpG1yInspProCysAla1eThrAr	260
Db	756	TTGTACACAGTCTCTTCAAGGATTAATCTCCGGGTGACAGATCCGTGTGCATACCCG	815
Oy	260	gLyseProG1yValYrThrlyVsValCyslystYrVal	272
Db	816	AAAGCTGTGTCTACACGAAAGTGTGCAAAATATGTG	852
RESULT 5			
LOCUS	AK009360	1295 bp	mRNA
DEFINITION			linear
			HTC 05-DEC-2002
			Mus musculus adult male tongue cDNA, RIKEN full-length enriched
			library, clone:2310015108 product:protease, serine, 20, full insert
			sequence.
ACCESSION	AK009360		
VERSION	AK009360.1	GI:12844110	
KEYWORDS			HTC; CAP trapper.
SOURCE			Mus musculus (house mouse)
ORGANISM			Mus musculus
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
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AUTHORS			
TITLE			
JOURNAL			
MEDLINE			

JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	2108560
PUBMED	11217851
REFERENCE	5
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
REFERENCE	Nature 420, 563-573 (2002)
AUTHORS	Adachi,T., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F., Imotani,K., Ishii,Y., Itch,M., Izawa,M., Katsukawa,T., Kato,H., Kawai,I., Koike,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishii,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Saeki,D., Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toyra,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp).
COMMENT	URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAAGAGATCGATCAAGACCTCTTTTCTTTTTTAA 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAAGATTCGATTATAAATTAATCCCCCCCCC 3']. cDNA was cleaved with XhoI and SctI. Cloning sites, 5' end: XhoI, 3' end: SctI. Host: SOLR.
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	/clone="2310015108"
	/sex="male"
	/tissue_type="tongue"
	/clone_lib="RIKEN full-length enriched mouse cDNA library"
	/dev_stage="adult"
	144..974
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	1277..1282
	/note="putative"

polyA_site 1295

/note="putative"

BASE COUNT 311 a 369 c 315 g 300 t

ORIGIN

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US-09-856-320A-2 (1-282) x AK009360 (1-1295)

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DB 186 AGGGAACCTGGCGCCGCCCTCCCTACTCCAGGCCAGATATTCTCCGACTCATTTGCA 245
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QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 366 GCAACCTCATGCGCCCAATGGCTCTCGACAGCAGCCACTGCGCGCAAGCCCATTAAC 425
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyGlyGlyGlyGlyGly 120
DB 426 GTGATCTCTTGGAGACCAATCTAGAGAGACAGAGCGCTGTAGCAGAGCGGATG 485
QY 121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
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LOCUS	AK009720	
DEFINITION	AK009720.1 GI:12844688	
ACCESSION	AK009720	
VERSION	AK009720.1	
KEYWORDS	HTC; CAP trapper.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	Carninci, P. and Hayashizaki, Y.	
TITLE	High-efficiency full-length cDNA cloning	
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE	99279253	
PUBMED	10349636	
REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	
TITLE	Genome Res. 10 (10), 1617-1630 (2000)	
JOURNAL	20499374	
MEDLINE	11042159	
PUBMED		
REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, U., Nishi, K., Kitunai, T., Tashtiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Macsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E., Matsumi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzaki, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	
TITLE	Genome Res. 10 (11), 1757-1771 (2000)	
JOURNAL	20530913	
MEDLINE	11076861	
PUBMED		
REFERENCE	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aikawa, K., Iwawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Tomita, M., Quackenbush, J., Schriml, L.M., Stebbins, F., Suzuki, K., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, D., Barsby, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, D., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyokawa, K., Wang, K.H., Weitz, C., Wiltaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)	
TITLE	Functional annotation of a full-length mouse cDNA collection	
JOURNAL	Nature 409 (6821), 685-690 (2001)	
MEDLINE	21085660	
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TITLE		
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REFERENCE	Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, Y., Nishi, K., Katsuna, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishie, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwa, K., Yonidake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aikawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gotojori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kushii, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stabli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fleischer, C., Fujita, M., Gariboldi, M., Gusticich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyokawa, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S. and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	12085660
PUBMED	12117851
REFERENCE	6
AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanaagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shitaki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of

COMMENT

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsunumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGCAGAGAGCATCCACAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGCAGAGCATTCGAGTTATTAATTAATATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI, 3' end: SstI.

Host: SOLR.

FEATURES

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/note="putative"

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BASE COUNT

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ORIGIN

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Best Local Similarity:

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US-09-856-320A-2 (1-282) x AK009659 (1-1269)

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QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100

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US-09-856-320a-2 (1-282) x BG697071 (1-708)

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DB 142 GCTCTGGCAACAGGGCTTGAGGGGAGACACAGATCTCAAGGGGTTGAGTCAAG 201
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VERSION BE867930.1 GI:10316706
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Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 973)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC

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CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM9562 row: a column: 06
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ORIGIN

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Alignment Scores:

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 Best Local Similarity: 81.75% Mismatches: 32
 Query Match: 67.04% Indels: 11
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US-09-856-320a-2 (1-282) x BE867930 (1-973)

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QY 1 MetG1nArgLeuArgTrpLeuArgAspTrpLysSerSerG1yArgG1yLeuThra1a1a 20
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QY 21 LysG1uProG1yAlaArgSerSerProLeuGlnAlaMetArg1LeuGlnLeu1Leu 40
DB 158 AAGGAACCTGGGGCCCGCTCTCCCGCCAGGCATAGATTCGACGTTAATCTCG 217
QY 41 LeuAlaLeuAlaThr-G1yLeuValG1yG1y---G1uTrArg1Le1e1yG1yPheG1 59
DB 218 CTGCTCTGGCAACAGGGCTGTGTAGGGGAGAGACACAGATCATCATCAAGGGGTTCCA 277
QY 59 uCysLysProH1SerGlnProTPrGlnAlaAlaLeuPheG1uLysThrArgLeuLeuCy 79
DB 278 GTGCAAGCTCATCTCCAGCCCTGGCAGGACGCCCTGTTCAAGAGAGCCGGCTACTCTG 337
QY 79 G1yAlaThrLeu1Lea1aProArgTrpLeuLeuThra1aAlaH1eCysLeuLysPro-- 98
DB 338 TGGGGCGAGCTCATGCGCCCGAGATGGCTCTGACAGACGCCCACTGCTCAAGCGCTG 397
QY 99 --ArgTrp1LeuValH1eSenLeuGlnH1aSenLeuGlnLysG1yG1yG1yG1yG1yG1y 118
DB 398 GCCGCTACATGTTACCTGGGGAGACACACCTCCAGAGAGAGAGGCTGTGAGCACA 457
QY 118 hrArgThra1aThrc1yLeuSerPheProH1SerProG1yPheAsnAsnSerLeuProAsnLys 138
DB 458 CCCGAGACGACCTAGTCTTCCCGCCCAACCCGGCTTCAACACAGAGCTCCCGCAGGAAG 517
QY 138 sPh1aArgAsnAsp1LeuMetLeuVal1yMetAlaSerProValSer1eThrTrpAla1y 158
DB 518 ACCACCGCAAGTACATGCTGTGAGAGATGCAATCCGCACTTCATCACCCTGGGCTG 577
QY 158 a1ArgProLeuThrLeuSerSerArgCysValThra1aG1yThrSerCysLeu1LeSerG 178
DB 578 TGGAGCCCTC-ACCTCTCTCATCGCTGTACTGTGGACACGAGTGCCTCATATTTCCG 636
QY 178 1yTrp-G1ySerThr-SerSerProG1nLeuArgLeuProH1SerThrLeuArgCysAla1a 197
DB 637 GCTGGGGCAGACAGTCAAGCCCGCACTTACGCTGCTCACACCTTGCGATGGGCCAA 696

```

QY	197	nlhehrjleilegihuhisglinlyescyluslnusnlatyrproglyasnilethrasph	217
Db	697	CAATACATCATATAGACACCAAAAGGTGATGAAACGATACCCGGCAACATTAACAGACAC	756
QY	217	lmevalcys-alaSERVALGIngluglyLYLysAspserCysgInglyAspserglyG	237
Db	757	CATGTGTGTTCACGACCTGACAGAGGGGGCACCGGATCATCTGCCAAGGTGAGCCCGGGG	816
QY	237	lyProleuValLysasnGlnserLeuGInglylIleleSerTrpGlyGlnAspProGlyA	257
Db	817	AGCCACTGGCGCTGTACACAGCCCGC-AAAAGGA--TAACTCCGGGGCAGACACCGATG	872
QY	257	laileThrArglyspProcglyValTYrThnLys	267
Db	873	CG--ACACCGGAAGCTGAGTTACCAAAAAG	901
RESULT 12			
LOCUS	BG747134	639 bp	mRNA
DEFINITION	602704354F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857733 5',		
ACCESSION	BG747134		
VERSION	BG747134.1	GI:14057787	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 639)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contract: Robert Strausberg, Ph.D. Email: cgeaphs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Place: LNCMI710 row: k column: 14 High quality sequence stop: 638. Location/Qualifiers 1..639 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4857733" /tissue_type="adenocarcinoma cell line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 15" /note="Organ: colon; Vector: pONT7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"		
BASE COUNT	128 a	241 c	162 g
ORIGIN			108 t
Alignment Scores:			
Pred. No.:	3,24e-80	Length:	639
Score:	975.00	Matches:	187
Percent Similarity:	97.47%	Conservative:	1
Best Local Similarity:	96.94%	Mismatches:	1
Query Match:	64.02%	Indels:	1
DB:	10	Gaps:	0

QY	22	GlupProglYAlaArgSerSerProleuInlameAArgileleuGlLeuileu	41
Db	73	GAACGTGGGGCCCGCTCTCTCCCTCCAGGCAATGAGATTTCGACTTAATCTGCT	132
QY	42	AlaLeuAlaThrGlyLeuValGlyGluThrArgIlelleleGlyPheGluCysLeys	61
Db	133	GCTCTGGCAACAGGGCTTGTAAGG-GGAAGACACAGAGATCATCAAGGGGTTCCAGTGGCAAG	191
QY	62	ProHisSerGlnProTArgAlaAlaIleuPheGluysThrArgLeuLeuCysGlyla	81
Db	192	CCTCACTCCAGCCCTGGCAGAGCCCTGTTCAAGAAAGACGGGCTACTGTGGGGG	251
QY	82	ThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyrIle	101
Db	252	ACGCTCATCGCCCCCAAGTGGCTCTCTGACACAGCCCACTGCTCAACCCCGGCTACATA	311
QY	102	ValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThrAla	121
Db	312	GTTCAACCTCGGGGAGCAGCACACCTCCAGAGAGAGGGGCTGTGACACACCCGGACAGC	371
QY	122	ThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArgAsn	141
Db	372	ACTGAGTCTTCCCCCACCCTCCGCTTCAACAACAGCTTCCCAACAAAGACACCGGCAT	431
QY	142	AspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgProLeu	161
Db	432	GACATCATGCTGGTGAAGATGGCATCGCCAGTCTCATCACCTGGGCTGTGGACCCCTC	491
QY	162	ThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrPglYser	181
Db	492	ACCTCTCTCCAGCGTGTGTACCTGGTGGACACAGCTCCCTCATTTCCGGCTGGGGCAGC	551
QY	182	ThiSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIleIle	201
Db	552	ACGTCACAGCCCCCAAGTTACGCTTGCCTGCATCACTTGGCATGCGCAACATCACATCAT	611
QY	202	GluHisGlnLysCysGluAsnAlaTyr	210
Db	612	GAGCACCGAAGTGTGAGACGCGCTAC	638
RESULT 13			
BM837078		539 bp	mrna
LOCUS			linear
DEFINITION	K-EST0113029 S9SNU601 Homo sapiens cDNA clone S9SNU601-64-B01 5',		EST 06-MAR-2007
ACCESSION	BM837078		
VERSION	BM837078.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 539) Kim,M.S., Hann,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.O., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S. 21C Frontier Korean EST Project 2001		
TITLE	Unpublished		
JOURNAL	Contact: Kim YS		
COMMENT	Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoseun-dong Yuseong-gu, Daejeon 305-353, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.krribd.re.kr Plate: 64 row: B column: 01 High quality sequence stop: 539. Location/Qualifiers 1..539 /organism="Homo sapiens" /mol_type="mrna" /db_xref="taxon:9606"		
FEATURES			
source			

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/clone="S9SNU601-64-B01"
/sex="M"
/issue_type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-601"
/lab_host="TopioF"
/clone_lib="S9SNU601"
/notes="Organ: Stomach; Vector: pME18-FLJ; Site 1: XhoI;
Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deacapped
with tabacco acid pyrophosphatase (TAP). The deacapped
intact mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of 14 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dt primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with SfiI and
cloned into DraIII-digested pME18s-FLJ vector. The
obtained cDNA vectors were used for transfection of
competent cells E. coli TopioF by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

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BASE COUNT      106 a      204 c      139 g      90 t
ORIGIN
Alignment Scores:
Pred. No.:      1,31e-65      Length:      539
Score:          816.00      Matches:      154
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    53.58%      Indels:      0
DB:             12      Gaps:      0

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US-09-856-320A-2 (1-282) x BM637078 (1-539)
QY      22 GIUPTGGIYALAAAGSERSERPROLEUGINALAMETARGILEUENLEULEU 41
DB      77 GAACCTGGGGCCGGCTCTCCCTCCAGGCATAGAGTTCTCGATTATCCGCTT 136
QY      42 AIALEUALATHGILYUENVALGILYUENRARGILELLEYSGLYUENGLYUEN 61
DB      137 GCTCTGGCAACAGGGCTTGTAGGGGAGACAGCATCATCAGGGGTTCCAGTCCAA 196
QY      62 PROHISSESGINPROTRPGINALAALAEUPHEGLULYVSTHARGLEUENYSGIYALA 81
DB      197 CCTCACTCCCAAGCCCTGGAGGAGCCCTGTTGAGAAAGACGGGGCTACTGTGGGGCG 256
QY      82 THLEULIeAlAPROARGTTRPLEUENUTRALAALAHISCYSEULYSPROARGTYRILE 101
DB      257 AGGCTCATGGCCCCCGATGGCTCCGACAGACAGCCCACTGCTCAAGCCCGCTACATA 316
QY      102 VALHISLEUGLYGINHISANLEUGINLYSGIUGIUGIYCYSGIUGINTHARGTHALA 121
DB      317 GTTCACTCTGGGGAGACCACTCCAGAAAGAGAGAGGCTGTAGACAGACCCGAGACGC 376
QY      122 THNGUSERPHEPROHISPROGLYPHEAANAENSERLEUPROASNLYSAPHISARGAAN 141
DB      377 ACTGAGCTCTTCCCAAGCCCGCTTCAACAACAGCTCCCAACAAGACCAAGCCGCAAT 436
QY      142 ASPILEMETLEUVALIYSMETALASERPROVALISERILETHTRPALAVAIARPPROLEU 161
DB      437 GACATCATCTGCTGTAAGATGCGCATGCGCAAGTCTCATCATCCTGGGCTGTGACACCCCTC 496
QY      162 THRLUSERSERARGCYSAIATHRALAGIYTHRSERYSEU 175
DB      497 ACCCTCTCTCAAGCTGTGTCACTGCTGACACAGCTGCCTC 538

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RESULT 14
LOCUS      B1046611      579 bp      mRNA      linear      EST 14-JUN-2001
DEFINITION MR3-FN0206-070201-013-e10 FN0206 Homo sapiens cDNA, mRNA sequence.
ACCESSION  B1046611
VERSION    B1046611.1  GI:14453233

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```

KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 579)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
          Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
          Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
          Brunstein,A., deoliveira,P.S., Bucher,P., vongenael,C.V., O'Hare
          ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
          Simpson,A.J.
          Shotgun sequencing of the human transcriptome with ORF expressed
          sequence tags
          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
          20202663
JOURNAL   MEDLINE
PUBMED    10737800
COMMENT   Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the PAPESP/LICR Human Cancer Genome
          Project. This entry can be seen in the following URL
          (http://www.ludwig.org.br/scripts/gethtml2.pl?c1=MR3&c2=MR3-FN0206-
          070201-013-e10&c3=2001-02-07&c4=1)
          Seq primer: puc 18 forward
          High quality sequence stop: 393.

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FEATURES
source
location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FN0206"
/notes="Organ: prostate normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

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BASE COUNT      121 a      180 c      172 g      106 t
ORIGIN
Alignment Scores:
Pred. No.:      1.59e-63      Length:      579
Score:          794.00      Matches:      164
Percent Similarity: 89.36%      Conservative: 4
Best Local Similarity: 87.23%      Mismatches: 16
Query Match:    52.13%      Indels:      6
DB:             12      Gaps:      1

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US-09-856-320A-2 (1-282) x B1046611 (1-579)
QY      1 METGINARGLEUARGTRPLEUARGSPTRYSSERSERGIYARGIYLEUTHRALA 20
DB      16 TTGCAGAGTTCAGAGTGGCTCGGGAGCTGGAAGTATCGGAGAGAGTCTCACACAGCC 75
QY      21 LYSGLUPROGLYALAAAGSERSERPROLEUGINALAMETARGILEUENLEULEU 40
DB      76 AAGGAACCTGGGGCCGGCTCTCCCTCCAGGCGCAAGAGATTCTCAGTTAATCTCTG 135
QY      41 LEUALALEUALATHGILYUENVALGILYUENRARGILELLEYSGLYPHEGLUCYS 60
DB      136 CTTCCTCTGTCAACAGGCTTGTAGGGGAGAGACCAAGATCATCAAGGGGTTCCAGTGC 195
QY      61 LYSPROHISSESGINPROTRPGINALAALAEUPHEGLULYVSTHARGLEUENYSGIY 80
DB      196 AAGCTCACTCCCAAGCCCTGGAGGACAGCGCTGTTGGAAGATGCGGCTACTGTGGG 255

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QY      81 AAThTleuIleAlAProArTrTpleuLeuThraIaAlaHiCysleuLysProArGTr 100
Db      256 GGGAGCGCTATGCCCCCGATGGCTCCCGAGACAGACCCACTGCTCAAGCCCCGCTAC 315
QY      101 ILeValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnThrArgTr 120
Db      316 ATAGTTCACCTGGGGGAGACACAACTCCGAAAGAGAGAGGCTGTGAGACAGACCGGACA 375
QY      121 AAThGUserPheProHisProGlyPheAsnAsnSerLeu-ProAsnLysAspHisAr 140
Db      376 GCCACTGAGTCTCTCCCCCAGCCGGGATTCAACAAGAGGCTCCCCAAAAAGACCACTG 435
QY      140 GAsnAspIleMetLeuValLysMetAlaSerProVal-SerIleThr-TpAlaValArg 159
Db      436 CAATGACATCATGCTGGTGAAGATGAGCATGGCCAGTCTTCATCACTTGCGCTGGGGA 495
QY      160 ProlauThleuSerSerArgCysValThraIaGlyThrSerCysleuIleSerGlyTrp 179
Db      496 CCCCTCAA-CTCTCTCAAGCTGTGT-ACTGCTGGCCAGCTGCTCATTTTC--GGCTGG 550
QY      180 GlySerThrSerSerPro 185
Db      551 GGGCAGACCTCAGCCCA 568

RESULT 15
LOCUS   BM982377.1 761 bp mRNA linear EST 21-FEB-2003
DEFINITION UI-CF-EN1-acs-o-17-0-UI-s1 UI-CF-EN1 Homo sapiens CDNA clone
VERSION  BM982377
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 761)
AUTHORS  Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE     Normalization and subtraction: two approaches to facilitate gene
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED    8889548
COMMENT   Contact: McCray, PB
          University of Iowa
          2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
          Tel: 319 356 4866
          Fax: 319 356 7171
          Email: paul-mccray@uiowa.edu
          Tissue Procurement: Dr. M. J. Welsh, University of Iowa
          CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
          CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Genetics (www.iresgen.com) or from Open Biosystems
          (www.openbiosystems.com).
          The following repetitive elements were found in this CDNA
          sequence: 17-100, >LINE2 (matched complement)
          Seq primer: M13 FORWARD
          POLY(A)=yes.

FEATURES
Source    1..761
           Location/Qualifiers
           1..761
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /clone="UI-CF-EN1-acs-o-17-0-UI"
           /tissue_type="Primary Lung Cystic Fibrosis Epithelial
           Cells"
           /dev_stage="Adult"
           /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
           /clone_lib="UI-CF-EN1"

```

```

/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I.
UI-CF-EN1 is a normalized CDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pRTT3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (d)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG_Lib=UI-CF-EN1
TAG_Tissue=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_SEQ=CTGCTCAGGT"

BASE COUNT  172 a 170 c 222 g 195 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 4,73e-62 Length: 761
Score: 780.00 Matches: 143
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 1
Query Match: 51.21% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2 (1-282) x BM982377 (1-761)
QY      139 HisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTpAlaVal 158
Db      761 CACGCAATGACATCATGCTGTGGAAGATGGCATCGCAGTCTCATCATCTGGGCTGTG 702
QY      159 ArgProLeuThrLysSerSerArgCysValThraIaGlyThrSerCysleuIleSerGly 178
Db      701 CGACCCCTCACCTCTCTCTCAAGNTGTCTACTGTGGACCACTGCTCATTTCCGGC 642
QY      179 TrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIle 198
Db      641 TGGGGACACAGTCACAGCCCGGAGTACGCTGCTCACACCTTGCGATGGCCAACTC 582
QY      199 ThrIleIleGluHisGlnLysCysGluAsnAlaIleTrpProGlyAsnIleThrAspThrMet 218
Db      581 ACCATCATTTGACACCAAGATGTGAGAACCCCTAACCCCGCAATCAGACACCATG 522
QY      219 ValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyPro 238
Db      521 GTGTGTGCCACGCTGCAGAAAGGGGCAAGGACTCTGCGAGGTACTCCGGGGCCCT 462
QY      239 LeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIle 258
Db      461 CTGGCTGTATACAGTCTCTTCAAGGCAATATCTCTCGGGGCCAGATCCGTGTGCGATC 402
QY      259 ThrArgLysProGlyValIleThrLysValCysLysIleValAspTrpIleGlnGluThr 278
Db      401 ACCGGAAGCCTGGTGTCTTACACCAAGTGTGAAATATGTGAGCTGATTCAGAGACG 342
QY      279 MetLysAsnAsn 282
Db      341 ATGAAAGAAACAT 330

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Search completed: October 23, 2003, 19:18:40
Job time : 2437.21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2003, 15:46:12 ; Search time 34.0587 Seconds
(without alignments)
1067.227 Million cell updates/sec

Title: US-09-856-320a-2_COPY_54_282
Perfect score: 1258
Sequence: 1 IIKGFCECKHSPQWQALFE.....GYTVKVKYDVIQETMKNN 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	100.0	250	21	Human TLSF. Homo
2	1258	100.0	250	21	Human PRO1279 (Homo)
3	1258	100.0	250	22	Human secreted pro
4	1258	100.0	250	22	Human PRO1279 poly
5	1258	100.0	250	22	Protein of the inv
6	1258	100.0	250	23	Prostate cancer as
7	1258	100.0	250	23	Human angiotensin
8	1258	100.0	250	23	Human PRO1279 prot
9	1258	100.0	250	23	Human PRO protein,

10	1258	100.0	250	24	ABU66822
11	1258	100.0	250	24	ABU67098
12	1258	100.0	250	24	ABU59903
13	1258	100.0	250	24	ABU56739
14	1258	100.0	282	20	AAV42439
15	1258	100.0	282	21	AAH11712
16	1258	100.0	282	21	AAV43636
17	1252	99.5	281	20	AAV42440
18	1235.5	98.2	275	21	AAH11714
19	1231	97.9	228	21	AAH21312
20	1228	97.6	250	20	AAV36093
21	1227	97.5	248	22	AAE08017
22	1219.5	96.9	289	21	AAH6483
23	1219.5	96.9	289	22	AAH67543
24	1062	84.4	276	21	AAH1713
25	1014.5	80.6	247	23	ABG70276
26	736	58.5	250	21	AAH21298
27	736	58.5	250	23	ABP64969
28	736	58.5	251	22	AAU16971
29	734	58.3	247	22	AAU23217
30	731.5	58.1	296	21	AAH21297
31	716	56.9	247	22	AAU86677
32	716	56.9	247	22	AAU23752
33	716	56.9	247	22	AAU17043
34	688	54.7	275	21	AAH21311
35	684	54.4	260	17	AAW10694
36	684	54.4	260	18	AAW12393
37	684	54.4	260	23	ABH57219
38	682	54.2	256	23	AAU79390
39	682	54.2	320	23	AAE19166
40	682	54.2	320	23	AAU82732
41	681	54.1	260	20	AAV41744
42	681	54.1	260	20	AAV32852
43	681	54.1	260	20	AAV03220
44	681	54.1	260	20	AAW87703
45	681	54.1	260	21	AAH21322

ALIGNMENTS

RESULT 1	AAH21325	strand: protein; 250 AA.
AC	AAH21325;	
DT	02-FEB-2001 (first entry)	
DE	Human TLSF.	
KW	Human; KIK-L1; KIK-L2; KIK-L3; KIK-L4; KIK-L5; KIK-L6; TLSF;	
KW	lysylsine-like serine protease; kallikrein-like protein; serine protease;	
KW	cytostatic; cancer; prostate cancer.	
OS	Homo sapiens.	
PN	WO200053776-A2.	
PD	14-SEP-2000.	
PF	09-MAR-2000; 2000WO-CA00258.	
PR	11-MAR-1999; 99US-0124260.	
PR	01-APR-1999; 99US-0127386.	
PR	21-JUL-1999; 99US-0144919.	
PA	(MOUNT) MOUNT SINAI HOSPITAL.	
PI	Yousef GM, Diamandis EP;	
DR	WPI, 2000-587440/55.	

PT New kallikrein-like (KLK-L) proteins for diagnosing and creating KLK-L
PT protein mediated disorders, especially cancer.
XX
PS Example 5; Fig 27; 184pp; English.
XX
CC The present sequence is human trypsin-like serine protease (TLSP), a
CC member of the serine protease family. Kallikreins and
CC kallikrein-like proteins are a subgroup of the serine protease enzyme
CC family. They catalyse the selective cleavage of specific polypeptide
CC precursors to release peptides with potent biological activity. Nucleic
CC acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4,
CC KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the
CC treatment, monitoring and diagnosis of cancers, especially prostate
CC cancer. They can also be used to identify a substance that can associate
CC with or mediate the biological activity of the proteins. Antibodies can
CC be used to treat conditions mediated by the kallikrein-like proteins.
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 6,3e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECRPHSQPMQAALEKTRRLCGATLIPRWLTPLTAHCKRPRIYVHGOHLOKEE 60
DB 22 IIKGFECRPHSQPMQAALEKTRRLCGATLIPRWLTPLTAHCKRPRIYVHGOHLOKEE 81
QY 61 GGEQRTATSPFPHGPNNSLPNKDRNDIMLVKASPVSIWAVRPPLTSSRCVTAGTS 120
DB 82 GGEQRTATSPFPHGPNNSLPNKDRNDIMLVKASPVSIWAVRPPLTSSRCVTAGTS 141
QY 121 CLISWGSTSPQLRLPHTLRCAITITIEHOKCENAVPNCITDTWVCASVQEGKDCSCG 180
DB 142 CLISWGSTSPQLRLPHTLRCAITITIEHOKCENAVPNCITDTWVCASVQEGKDCSCG 201
QY 181 DSGGLPVCNQSLOGIISWGQDCATTRKGVYTKYCKVYDWIOETMKNN 229
DB 202 DSGGLPVCNQSLOGIISWGQDCATTRKGVYTKYCKVYDWIOETMKNN 250

RESULT 2
AAV99390 standard; Protein; 250 AA.
XX
AC AAV99390;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1279 (UNO649) amino acid sequence SEQ ID NO:170.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
FN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20111.
XX
PR 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.
PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.

PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 10-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100587.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102310.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103637.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105002.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 21-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.

PR 27-OCT-1998; 98US-0105881.
 PR 27-OCT-1998; 98US-0105882.
 PR 27-OCT-1998; 98US-0106062.
 PR 28-OCT-1998; 98US-0106023.
 PR 28-OCT-1998; 98US-0106029.
 PR 28-OCT-1998; 98US-0106030.
 PR 28-OCT-1998; 98US-0106032.
 PR 28-OCT-1998; 98US-0106033.
 PR 28-OCT-1998; 98US-0106178.
 PR 29-OCT-1998; 98US-0106248.
 PR 29-OCT-1998; 98US-0106384.
 PR 29-OCT-1998; 98US-0108500.
 PR 30-OCT-1998; 98US-0106464.
 PR 03-NOV-1998; 98US-0106856.
 PR 03-NOV-1998; 98US-0106902.
 PR 03-NOV-1998; 98US-0106905.
 PR 03-NOV-1998; 98US-0106919.
 PR 03-NOV-1998; 98US-0106932.
 PR 03-NOV-1998; 98US-0106934.
 PR 10-NOV-1998; 98US-0107783.
 PR 17-NOV-1998; 98US-0108775.
 PR 17-NOV-1998; 98US-0108779.
 PR 17-NOV-1998; 98US-0108787.
 PR 17-NOV-1998; 98US-0108788.
 PR 17-NOV-1998; 98US-0108801.
 PR 17-NOV-1998; 98US-0108802.
 PR 17-NOV-1998; 98US-0108806.
 PR 17-NOV-1998; 98US-0108807.
 PR 17-NOV-1998; 98US-0108867.
 PR 17-NOV-1998; 98US-0108925.
 PR 18-NOV-1998; 98US-0108848.
 PR 18-NOV-1998; 98US-0108849.
 PR 18-NOV-1998; 98US-0108850.
 PR 18-NOV-1998; 98US-0108851.
 PR 18-NOV-1998; 98US-0108852.
 PR 18-NOV-1998; 98US-0108858.
 PR 18-NOV-1998; 98US-0108904.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 XX
 DR WPI; 2000-237871/20.
 DR N-PSDB; AAA37072.
 XX
 PT New mammalian DNA sequences encoding transmembrane, receptor or
 PT secreted PRO polypeptides, useful for screening of potential peptide or
 XX small molecule inhibitors of the relevant receptor/ligand interactions
 XX
 PS Claim 12; Fig 102; 773pp; English.
 XX
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AAY9340 to AAY9462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding then have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
 CC PCR primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention.
 XX
 SO Sequence 250 AA.

Query Match 100.0%; Score 1258; DB 21; Length 250;
 Best Local Similarity 100.0%; Pred. No. 6,3e-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECRKHSPQWQALFEKTRLLCGATLTPRWLLTAHCLKRRIYVHLGQNLQKEE 60
 DB 22 IIKGECRKHSPQWQALFEKTRLLCGATLTPRWLLTAHCLKRRIYVHLGQNLQKEE 81
 QY 61 GGEOTRTATESFPHDPFNNSLPNKHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
 |||

DB 82 GGEOTRTATESFPHDPFNNSLPNKHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
 QY 121 CLISGWSSTSSPOLPLPHTLRCAITITIEHQECENAYRPNIIDTWVCASVQGGKDS 180
 DB 142 CLISGWSSTSSPOLPLPHTLRCAITITIEHQECENAYRPNIIDTWVCASVQGGKDS 201
 QY 181 DSGGPLVNCQSLQGIISWQDPCATRKRGVYTKCKYVDWIQETMKNN 229
 DB 202 DSGGPLVNCQSLQGIISWQDPCATRKRGVYTKCKYVDWIQETMKNN 250

RESULT 3
 ABB50479
 ID ABB50479 strand; Protein; 250 AA.
 XX
 AC ABB50479;
 XX
 DT 07-FEB-2002 (first entry)
 XX
 DE Human secreted protein encoded by gene 179 SEQ ID NO:427.
 XX
 KW Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
 KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 KW cytosolic; cardiac; vascular; anti-angiogenic; ophthalmological;
 KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnary;
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
 KW Gaucher's disease; cardiovascular disease; Schmitz syndrome; chemotaxis;
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;
 KW Parkinson's disease; infectious disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200162891-A2.
 XX
 PD 30-AUG-2001.
 XX
 XX 21-FEB-2001; 2001WO-US05614.
 XX
 PF 24-FEB-2000; 2000US-184836P.
 PR 29-MAR-2000; 2000US-193170P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P;
 PI Feng P, Endress GA, Dillon PU, Carter KC, Brewer LA, Yu G;
 PI Zeng Z, Greene JM;
 XX
 DR WPI; 2001-625724/72.
 DR N-PSDB; ABA83372.
 XX
 PT Nucleic acids encoding 207 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX
 PS Claim 11; Page 1181-1182; 1533pp; English.
 XX
 CC ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.
 CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 CC anti-HIV; cytosolic; cardiac; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
 CC antiparkinsonian; antimicrobial; and vulnary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus

CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABB83185 to
 CC ABB83193 and ABB80300 represent sequences used in the exemplification of
 CC the present invention.

XX Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 6.3e-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIKGFECKPHSQPQOALFEKTRLLCGATLTPRWLLTAHCLKPRIVVHGGNHLQKEE 60
 Db 22 IIKGFECKPHSQPQOALFEKTRLLCGATLTPRWLLTAHCLKPRIVVHGGNHLQKEE 81
 Qy 61 GCEQTRTATESFPHPGFNNLSLPNKHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 120
 Db 82 GCEQTRTATESFPHPGFNNLSLPNKHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 141
 Qy 121 CLISGWSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCASVOEGKDSGCG 180
 Db 142 CLISGWSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCASVOEGKDSGCG 201
 Qy 181 DSGGPLVNCNOSLOGIISWGODPCATTRKPGVYTKVCKYVDMIOETMKN 229
 Db 202 DSGGPLVNCNOSLOGIISWGODPCATTRKPGVYTKVCKYVDMIOETMKN 250

RESULT 4

AAU12424 standard; Protein; 250 AA.

XX AAU12424;
 XX 24-OCT-2001 (first entry)
 XX Human PRO1279 polypeptide sequence.
 XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.

OS Homo sapiens.
 XX WO200140466-A2.
 XX 07-JUN-2001.
 PD
 XX
 PE 01-DEC-2000; 2000WO-US32678.
 XX
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.

XX (GENTECH) INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI: 2001-408281/43.
 DR N-PSDB; AAS21496.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX Claim 12, Fig 506; 813pp; English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.

XX Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 6.3e-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIKGFECKPHSQPQOALFEKTRLLCGATLTPRWLLTAHCLKPRIVVHGGNHLQKEE 60
 Db 22 IIKGFECKPHSQPQOALFEKTRLLCGATLTPRWLLTAHCLKPRIVVHGGNHLQKEE 81
 Qy 61 GCEQTRTATESFPHPGFNNLSLPNKHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 120
 Db 82 GCEQTRTATESFPHPGFNNLSLPNKHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 141
 Qy 121 CLISGWSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCASVOEGKDSGCG 180
 Db 142 CLISGWSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCASVOEGKDSGCG 201
 Qy 181 DSGGPLVNCNOSLOGIISWGODPCATTRKPGVYTKVCKYVDMIOETMKN 229
 Db 202 DSGGPLVNCNOSLOGIISWGODPCATTRKPGVYTKVCKYVDMIOETMKN 250

RESULT 5

AAB66139

ID AAB6139 standard; protein; 250 AA.
XX
AC AAB6139;
XX
DT 02-APR-2001 (first entry)
XX
DE Protein of the invention #51.
XX
KW Secreted; transmembrane; gene therapy.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US04342.
XX
PR 23-JUN-1999; 99US-0141037.
XX
PR 20-JUL-1999; 99US-0144758.
XX
PR 26-JUL-1999; 99US-0145698.
XX
PR 01-SEP-1999; 99WO-US20111.
XX
PR 29-OCT-1999; 99US-0162506.
XX
PR 30-NOV-1999; 99WO-US28313.
XX
PR 02-DEC-1999; 99WO-US28551.
XX
PR 16-DEC-1999; 99WO-US30095.
XX
PR 05-JAN-2000; 2000WO-US00219.
XX
PR 06-JAN-2000; 2000WO-US00376.
XX
XX
XX (GENTH) GENENTECH INC.
XX
PI Baker KP, Borstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PI, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoletti NF, Roy MA, Smith V, Stewart TA, Tumas D;
PI Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2001-071395/08.
XX
PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy -
XX
PS Claim 1; Fig 102; 787bp; English.
XX
XX
XX The present invention relates to secreted and transmembrane proteins.
XX These proteins and the DNA encoding them may be used as hybridization
XX probes, in chromosome and gene mapping and in the generation of
XX anti-sense RNA and DNA. They may also be used to generate either
XX transgenic animals or knockout animals which are in turn useful for
XX development and screening of therapeutically useful reagents.
XX CC The nucleic acids may also be used in gene therapy.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 1258; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.3e-113; Indels 0; Gaps 0;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIKGECKRPHSQPWOALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
DB 22 IIKGECKRPHSQPWOALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
QY 61 GGEQRTATASFPHQGFNNLSLPHKDRNDIMLVKASPVSTWAVRPLTLSSRCTYAGTS 120
DB 82 GGEQRTATASFPHQGFNNLSLPHKDRNDIMLVKASPVSTWAVRPLTLSSRCTYAGTS 141
QY 121 CLISGSGTSSPOLRLPHTLRCANITIIHOKCENAYPNITPTWVCASVOGSGKDCOG 180
DB 142 CLISGSGTSSPOLRLPHTLRCANITIIHOKCENAYPNITPTWVCASVOGSGKDCOG 201
QY 181 DSGGPIVNCQSLGGIISWGQDPCATIRKPGVYTKVCKYVDWIQETMKN 229
DB 202 DSGGPIVNCQSLGGIISWGQDPCATIRKPGVYTKVCKYVDWIQETMKN 250

RESULT 6
ID AABG1816 standard; Protein; 250 AA.
XX
AC AABG1816;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated protein #17.
XX
DE Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
XX
KW Mammalia.
XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US32045.
XX
XX
XX 13-OCT-2000; 2000US-0687576.
XX
XX 08-DEC-2000; 2000US-0733288.
XX
XX 08-DEC-2000; 2000US-0733742.
XX
XX 24-JAN-2001; 2001US-263957P.
XX
XX 16-MAR-2001; 2001US-276791P.
XX
XX 16-MAR-2001; 2001US-276888P.
XX
XX 06-APR-2001; 2001US-281922P.
XX
XX 24-APR-2001; 2001US-286214P.
XX
XX 30-APR-2001; 2001US-0847046.
XX
XX 04-MAY-2001; 2001US-288589P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
XX WPI: 2002-471335/50.
XX
XX N-PSDB; ABK92131.
XX
XX
XX Detecting a prostate cancer-associated transcript in a cell in a
XX patient, useful for diagnosing prostate cancer (PC) or screening
XX PT modulators of PC, by determining if prostate cancer-associated genes
XX PT are expressed in a prostate tissue -
XX
XX
XX Claim 27; Page 314; 436bp; English.
XX
XX
XX The present invention relates to methods of detecting a prostate
XX cancer-associated transcript in a cell from a patient. The method
XX comprises contacting a biological sample from the patient with
XX CC prostate cancer-associated polynucleotides (designated PC genes) that
XX CC selectively hybridize to a sequence that is at least 80% identical
XX CC to them. The prostate cancer-associated polynucleotide sequences
XX CC are differentially expressed in prostate tumour tissue or in
XX CC prostate cancer and are derived from the tissues of various
XX CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
XX CC The methods of the invention are useful for diagnosing and treating
XX CC prostate cancer in mammals. The prostate cancer-associated genes are
XX CC useful for diagnosing or treating prostate cancer, as well as for
XX CC identifying modulators of prostate cancer or agents that inhibit
XX CC prostate cancer. The nucleic acid sequences are particularly useful
XX CC in gene therapy, as a vaccine or in antisense applications.
XX CC ABG61800-ABG61944 represent prostate cancer-associated proteins.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 1258; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.3e-113; Indels 0; Gaps 0;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIKGECKRPHSQPWOALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
DB 22 IIKGECKRPHSQPWOALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81

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QY 61 GCEQRTLTESFPHPGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 82 GCEQRTLTATESFPHPGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
QY 121 CLISGSGTSSPQLRPLHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGKDSOG 180
DB 142 CLISGSGTSSPQLRPLHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGKDSOG 201
QY 181 DSGGPLVNCOSLOGIISWGDPFCATIRKPGVYTKVCKYVDWIQETMKN 229
DB 202 DSGGPLVNCOSLOGIISWGDPFCATIRKPGVYTKVCKYVDWIQETMKN 250

RESULT 7
ABB95526
ID ABB95526 standard; Protein; 250 AA.
XX
AC ABB95526;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
XX
KM Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KM cardiac; cystostatic; antiangiogenic; hypotensive; vulnerary;
KM antiarteriosclerotic.
XX
OS Homo sapiens.
XX
FN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-064357.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242822P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US10952.
PR 10-NOV-2000; 2000WO-US10873.
PR 01-DEC-2000; 2000WO-US12678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001US-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-080689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.

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PR 28-JUN-2001; 2001WO-US00000.
XX
XX (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODDARD P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AU, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
DR MPI; 2002-171999/22.
DR N-FSDB; ABL95664.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 208; 567pp; English.
XX
XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention.
XX
XX Sequence 250 AA;
SQ
Query Match 100.0%; Score 1258; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.3e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIKGFCKPHSQPOMALFEKTRILCGATLAPRMLTAAHCLRPYIVHLGHNLOKEE 60
DB 22 IIKGFCKPHSQPOMALFEKTRILCGATLAPRMLTAAHCLRPYIVHLGHNLOKEE 81
QY 61 GCEQRTLTATESFPHPGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 82 GCEQRTLTATESFPHPGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
QY 121 CLISGSGTSSPQLRPLHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGKDSOG 180
DB 142 CLISGSGTSSPQLRPLHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGKDSOG 201
QY 181 DSGGPLVNCOSLOGIISWGDPFCATIRKPGVYTKVCKYVDWIQETMKN 229
DB 202 DSGGPLVNCOSLOGIISWGDPFCATIRKPGVYTKVCKYVDWIQETMKN 250

RESULT 8
ABB84920
ID ABB84920 standard; Protein; 250 AA.
XX
AC ABB84920;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1279 protein sequence SEQ ID NO:208.

```

XX Human; angiogenesis; cardiant; cytosolic; antiangiogenic; hypotensive;
 KW Vlnary; antarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US19692.
 XX
 XX 23-JUN-2000; 2000US-213637P.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222655P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-2429238.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Warsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 DR WPI; 2002-090516/12.
 DR N-PSDB; ABL88175.
 XX
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 11; Fig 208; 565pp; English.
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABL884817 to
 CC ABL88503. The PRO proteins and polynucleotides have cardiant, cytosolic,
 CC antiangiogenic, hypotensive, vlnary and antarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,

CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal.
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 XX
 XX Sequence 250 AA;
 SQ
 Query Match 100.0%; Score 1258; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred No. 6.3e-113; Gaps 0;
 Matches 229; Conservative 0; Mismatches 0; Indels 0;
 QY 1 IIKGFCKPSPQWQALFEKTRLLCGATLIPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
 DB 22 IIKGFCKPSPQWQALFEKTRLLCGATLIPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
 QY 61 GCEQRTATSPPHGFNNSLPNKQHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 120
 DB 82 GCEQRTATSPPHGFNNSLPNKQHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 141
 QY 121 CLISGSGTSSPOLRLPHTLRCAANTIIIEHCKENAYPENITDTWVCASVQEGSKDSCOG 180
 DB 142 CLISGSGTSSPOLRLPHTLRCAANTIIIEHCKENAYPENITDTWVCASVQEGSKDSCOG 201
 QY 181 DSGGPLVCNQSLOGIISWGQDPCATTRKPGVYTKYKVDWIQETMKN 229
 DB 202 DSGGPLVCNQSLOGIISWGQDPCATTRKPGVYTKYKVDWIQETMKN 250
 RESULT 9
 AAU83684
 ID AAU83684 standard; Protein; 250 AA.
 AC AAU83684;
 DT 08-MAY-2002 (first entry)
 DE Human PRO protein, Seq ID No 186.
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 OS Homo sapiens.
 PN WO200208288-A2.
 PD 31-JAN-2002.
 PF 29-JUN-2001; 2001WO-US21066.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX
 PA (GETH) GENENTECH INC.
 XX
 P1 Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
 P1 Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
 XX
 DR MPI; 2002-172001/22.
 DR N-PSDB; ARK33628.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 PS Claim 11; Figure 186; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for stimulating
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention.
 CC
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 1258; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 6,36-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IIKGECKPHSQWQALFEKTRLLCGATLIAPRLTLTAHCLKPRYIVHLGQHNLOKEE 60
 Db 22 IIKGECKPHSQWQALFEKTRLLCGATLIAPRLTLTAHCLKPRYIVHLGQHNLOKEE 81
 QY 61 GCEQRTATESPPHGFNNSLPNKDRNDIMLVKASVSTTWAAPRLTSSRCTACTS 120
 Db 82 GCEQRTATESPPHGFNNSLPNKDRNDIMLVKASVSTTWAAPRLTSSRCTACTS 141
 QY 121 CLISGSGTSSPOLRLPHTLRCANITITIEHOKCEAAYGNTITDTWVCASVOEGKDSQCG 180
 Db 142 CLISGSGTSSPOLRLPHTLRCANITITIEHOKCEAAYGNTITDTWVCASVOEGKDSQCG 201
 QY 181 DSGGELVNCOSLQGIISWGDPICALTRKPGYTVKVCYVDWIQETMKKN 229
 Db 202 DSGGELVNCOSLQGIISWGDPICALTRKPGYTVKVCYVDWIQETMKKN 250
 RESULT 10
 ABU66822
 ID ABU66822 standard; Protein; 250 AA.
 XX
 AC ABU66822;
 XX
 DT 23-MAY-2003 (first entry)
 XX
 DE Human PRO polypeptide #253.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;

KW differentiation; chondrocyte; tumour; genetic disorder;
 KW cytosolatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003036180-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 09-MAY-2002; 2002US-0143114.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10723.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 16-DEC-1999; 99WO-US28565.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US03376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.

28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Deenoyers L, Filvaroff E, Gao W,
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-332040/31.
 DR N-PSDB; ACA03855.
 XX
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification
 XX
 PS Claim 12; Fig 506; 660pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. AB066570-AB066844 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsdIdentify.html.

XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 1258; DB 24; Length 250;
 Best Local Similarity 100.0%; Pred. No. 6.3e-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY
 1 IIKGFCKRHSPQWQALFEKTRLLCGATLLIAPRWLLTTAAHCLKPRYIYHLCQHNQKE 60
 DB 22 IIKGFCKRHSPQWQALFEKTRLLCGATLLIAPRWLLTTAAHCLKPRYIYHLCQHNQKE 81
 QY 61 GCEQRTATESFPHPFNNSLPNKDRNDIMEVKMASPSITWAVPLTSSRCVAGTS 120
 DB 82 GCEQRTATESFPHPFNNSLPNKDRNDIMEVKMASPSITWAVPLTSSRCVAGTS 141
 DB 121 CLISGWSTSSPOLRLPHTLRCAANTIIEHCKENAYPGNITDTWVCASVQEGKDCSCG 180
 DB 142 CLISGWSTSSPOLRLPHTLRCAANTIIEHCKENAYPGNITDTWVCASVQEGKDCSCG 201
 QY 181 DSGGPLVCNOSLOGIISWGQDCATRRKPGVYTKCKYVDWIQETMKN 229
 DB 202 DSGGPLVCNOSLOGIISWGQDCATRRKPGVYTKCKYVDWIQETMKN 250
 RESULT 11
 AB067098
 ID AB067098 standard; Protein; 250 AA.
 XX
 AC AB067098;
 XX
 DT 27-MAY-2003 (first entry)
 XX
 DE Human secreted/transmembrane, PRO, protein SEQ ID 506.
 XX
 KW Human; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioreactor; tumour.
 XX
 OS Homo sapiens.
 OS
 XX
 PN US2003032155-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 03-MAY-2002; 2002US-0137865.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22992.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US00528.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28431.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23222.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-080689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0865028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.

PR 19-DEC-2001; 2001US-0028072.
XX
XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX WPI, 2003-331925/31.
DR N-PSDB; ACA04276.
XX
XX New secreted and transmembrane nucleic acids and polypeptides,
PT designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer
XX
XX Claim 12; Fig 506; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid
CC further comprises the full-length coding sequence of the DNA deposited
CC under American Type Culture Collection (ATCC) accession number in a list
CC given in the specification. Also included are vectors and host
CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
CC antibodies, PRO extracellular domains and mature sequences, methods
CC of detecting PRO proteins, methods for stimulating the release of
CC TNF-alpha (tumour necrosis factor alpha) from human blood,
CC (and the proliferation of differentiation of chondrocyte cells, the
CC proliferation of, or gene expression in pericyte cells, the release or
CC proteoglycans from cartilage, proliferation of inner ear utricular
CC supporting cells, the proliferation of T-lymphocyte cells, the release
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
CC proliferation of endothelial cells), a method for modulating the uptake
CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
CC a method for inhibiting the binding of A-peptide to factor VIIa,
CC or the differentiation of adipocyte cells, a method for detecting the
CC presence of a tumour in a mammal and an oligonucleotide probe derived
CC from any of the nucleotide sequences cited above. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
CC diabetic complications. The nucleic acids are useful as hybridisation
CC probes, in chromosome and gene mapping, and in generating antisense RNA
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors. Both are useful in tissue typing.
XX The present sequence represents a PRO protein of the invention.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 1256; DB 24; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.3e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIKGECKPHOPQALFEKTRLLCGATLAPRWLLTAACHLPRIYVHLGONLQKEE 60
DB 22 IIKGECKPHOPQALFEKTRLLCGATLAPRWLLTAACHLPRIYVHLGONLQKEE 81
QY 61 GCEQRTATSEFPHPGFNLSLPNKDRNDIMLVMAFVSITMAVRPLTSSRCTACTS 120
DB 82 GCEQRTATSEFPHPGFNLSLPNKDRNDIMLVMAFVSITMAVRPLTSSRCTACTS 141
QY 121 CLISGWSSTSPQRLPHTLRCAITITIEHCKENAVPGNITDTMVCASVEGKGDSOG 180
DB 142 CLISGWSSTSPQRLPHTLRCAITITIEHCKENAVPGNITDTMVCASVEGKGDSOG 201
QY 181 DSGGPLVNCOSLQGISWGQPCATIRKPGYTVCKVVDIOETMKN 229
DB 202 DSGGPLVNCOSLQGISWGQPCATIRKPGYTVCKVVDIOETMKN 250
RESULT 12

ABUS9903
ID ABUS9903 standard; Protein; 250 AA.
XX
AC ABUS9903;
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO1279.
XX
KW Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-0140808.
XX
PR 31-MAR-1997; 97WO-US05330.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22891.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28651.
PR 02-DEC-1999; 99WO-US28654.
PR 02-DEC-1999; 99WO-US28665.
PR 02-DEC-1999; 99WO-US28666.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0806889.
PR 22-MAR-2001; 2001US-0815744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
PA (GENTH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-148238/14.
XX N-PSDB; ABX89393.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
XX are therapeutically useful for enhancing immune response and in cancer
XX treatments -
XX
XX Claim 12; Fig 506; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
XX polypeptides are useful in detecting human PRO polypeptides in a sample, in
CC

CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO3943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO26,
CC PRO1068, PRO1184, PRO1366 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or Crohn's
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC is the amino acid sequence of a novel human PRO protein.

SQ Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 24; Length 250;

Best Local Similarity 100.0%; Pred. No. 6.3e-113;

Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPSPQWQALFEKTRLLCGATLAPRWMLTAHCLKPRIVYHVGQHNLOKEE 60
DB 22 IIKGECKPSPQWQALFEKTRLLCGATLAPRWMLTAHCLKPRIVYHVGQHNLOKEE 81

QY 61 GCEQTRTATESFPHPGNNNSLPNKHNDIMLVKASPVSTIWAIVPLTSSRCVTAGTS 120
DB 82 GCEQTRTATESFPHPGNNNSLPNKHNDIMLVKASPVSTIWAIVPLTSSRCVTAGTS 141

QY 121 CLISGWSSTSPQLRPHLTRCANITIEHOKCENAVPGNITDTMVCASVDEGKDSQCG 180
DB 142 CLISGWSSTSPQLRPHLTRCANITIEHOKCENAVPGNITDTMVCASVDEGKDSQCG 201

QY 181 DSGGPLVNCNOSLQGIISWGDPICATITRKPGVYTKVCKYVDWIOETMKN 229
DB 202 DSGGPLVNCNOSLQGIISWGDPICATITRKPGVYTKVCKYVDWIOETMKN 250

RESULT 13

ABUS6739 standard; Protein; 250 AA.

ID ABUS6739;

AC ABUS6739;

DT 02-APR-2003 (first entry)

DB Lung cancer-associated polypeptide #332.

QY Lung cancer-associated polypeptide; cytosolic; emphysema;

DB small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

QY chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

DB interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

QY Unidentified.

DB WO200286443-A2.

QY 31-OCT-2002.

XX

PF 18-APR-2002; 2002WO-US12476.
XX 18-APR-2001; 2001US-284770P.
PR 10-MAY-2001; 2001US-290492P.
PR 09-NOV-2001; 2001US-339245P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-NOV-2001; 2001US-334370P.
PR 12-APR-2002; 2002US-372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
PA Aziz N, Murray R;
XX WPI: 2003-093161/08.
DR N-PSDB; ABX76468.

Claim 27; Page 443-444; 453pp; English.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the invention.

SQ Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 24; Length 250;

Best Local Similarity 100.0%; Pred. No. 6.3e-113;

Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPSPQWQALFEKTRLLCGATLAPRWMLTAHCLKPRIVYHVGQHNLOKEE 60
DB 22 IIKGECKPSPQWQALFEKTRLLCGATLAPRWMLTAHCLKPRIVYHVGQHNLOKEE 81

QY 61 GCEQTRTATESFPHPGNNNSLPNKHNDIMLVKASPVSTIWAIVPLTSSRCVTAGTS 120
DB 82 GCEQTRTATESFPHPGNNNSLPNKHNDIMLVKASPVSTIWAIVPLTSSRCVTAGTS 141

QY 121 CLISGWSSTSPQLRPHLTRCANITIEHOKCENAVPGNITDTMVCASVDEGKDSQCG 180
DB 142 CLISGWSSTSPQLRPHLTRCANITIEHOKCENAVPGNITDTMVCASVDEGKDSQCG 201

QY 181 DSGGPLVNCNOSLQGIISWGDPICATITRKPGVYTKVCKYVDWIOETMKN 229
DB 202 DSGGPLVNCNOSLQGIISWGDPICATITRKPGVYTKVCKYVDWIOETMKN 250

RESULT 14

AA442439 standard; Protein; 282 AA.

ID AA442439;

AC AA442439;

DT 08-DEC-1999 (first entry)

```

XX CASB12 amino acid sequence.
DE
XX
XX neurospisin; cancer; assay; inhibitor; serine protease; immunogenic;
KM autoimmune disease.
XX
XX Homo sapiens.
OS
XX WO949055-A1.
PN
XX 30-SEP-1999.
PD
XX 17-MAR-1999; 99WO-EP01894.
PF
XX 20-MAR-1998; 98GB-0006095.
PR
XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX Bruck CEM, Caesart J, Coche T, Vinals-bassols C;
PI
XX WPI; 1999-580450/49.
DR
XX N-PSDB; AA222638.
DR
XX
XX New human serine protease CASB12, for treatment, prevention and
PT diagnosis of cancer and autoimmune diseases -
XX
XX Claim 3; Page 48; 58pp; English.
XX
XX This is the amino acid sequence of the CASB12 protein. The nucleotide
CC sequence of AA222638 shows homology with neuropilin and the encoded
CC protein AA42439 is structurally related to other proteins of the
CC serine protease family, having homology and/or structural similarity
CC with neuropilin. It is expected that as well as similar structure, these
CC proteins will also share similar biological functions and properties.
CC The CASB12 polypeptides and polynucleotides can be used to develop
CC methods for identifying agonists and antagonists/inhibitors of these
CC molecules, and thereby treating conditions associated with CASB12
CC polypeptide imbalance. The invention also provides for diagnostic assays
CC for detecting diseases associated with inappropriate CASB12 polypeptide
CC activity or levels.
CC Since CASB12 is either specifically expressed or highly over-expressed
CC in tumors compared to normal cells, the polypeptides and polynucleotides
CC of the invention are believed to be important immunogens for specific
CC prophylactic or therapeutic immunization against tumors. The
CC polypeptides and polynucleotides can therefore be targeted by antigen
CC specific immune reactions (which result in the destruction of the tumor
CC cell) or they can be used to diagnose the occurrence of tumor cells
XX
XX
XX Sequence 282 AA;
SQ
Query Match 100.0%; Score 1258; DB 20; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.4e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIKGFECKPHSQPQWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLCQHNLOKXE 60
DB 54 IIKGFECKPHSQPQWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLCQHNLOKXE 113
QY 61 GCEQRTTATESFPHPGFNNSLPNKDHNDIMLVKASPVSTWAVRPLTLLSRCTACTS 120
DB 114 GCEQRTTATESFPHPGFNNSLPNKDHNDIMLVKASPVSTWAVRPLTLLSRCTACTS 173
QY 121 CLISGSGTSSPOLRLPHTLRCAANTIIEHQKCNAYPGNITDTWVCASVOEGKDSGCG 180
DB 174 CLISGSGTSSPOLRLPHTLRCAANTIIEHQKCNAYPGNITDTWVCASVOEGKDSGCG 233
QY 181 DSGGPLVNCQSLQGIISWGQDPCATIRKPGVYTKYCKYVDMIQETMKNN 229
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AAB11712

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ID AAB11712 standard; Protein; 282 AA.
XX
XX AAB11712;
AC
XX
XX 23-OCT-2000 (first entry)
DT
XX
XX Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.
DE
XX
XX BSSP6; serine protease; human; hBSSP6; mouse; mBSSP6; brain;
KM diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
KM epilepsy; cancer; inflammation; infertility; pancreatitis;
KW prostatic hypertrophy.
XX
XX Homo sapiens.
OS
XX WO200031257-A1.
PN
XX 02-JUN-2000.
PD
XX 19-NOV-1999; 99WO-JP06476.
PF
XX 20-NOV-1998; 98JP-0347802.
PR
XX (FUSO ) FUSO PHARM IND LTD.
PA
XX
XX Uemura H, Okui A, Kominami K, Yamaguchi N, Mitsu S;
PI
XX WPI; 2000-400067/34.
DR
XX N-PSDB; AAA61763.
DR
XX
XX Serine protease BSSP6, useful in detecting homologs, mutants and
PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
PT epilepsy, cancer, inflammation, infertility and prostatic hypertrophy,
PT using blood or other tissues -
XX
XX Claim 1; Page 69-70; 94pp; Japanese.
XX
XX The invention relates to novel serine proteases designated BSSP6
CC (AAB11712-81114), and to nucleic acids encoding them (AAA61763-A61765).
CC The invention also relates to vectors and transformants comprising BSSP6
CC nucleic acids; transgenic animals in which the expression level of BSSP6
CC can be varied; and an mBSSP6 knockout mouse. The invention additionally
CC encompasses anti-BSSP6 antibodies and methods of production of such
CC antibodies, methods of BSSP6 detection using the antibodies, and the
CC use of BSSP6 proteins or fragments as diagnostic markers for certain
CC medical conditions. Nucleotides encoding BSSP6 were initially
CC isolated in a human brain cDNA library using degenerate PCR primers
CC (AAA61795-A61796) based on conserved regions of serine proteases. The
CC BSSP6 serine proteases and nucleotides encoding them are useful in
CC detecting homologues, mutants and polymorphic variants in biological
CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
CC and spleen) as diagnostic markers for conditions such as Alzheimer's
CC disease, epilepsy, cancer, inflammation, infertility and prostatic
CC hypertrophy. Sequences AAB11712 and AAB11714 represent human BSSP6
CC variants (hBSSP6), and sequence AAB11713 represents murine BSSP6
CC (mBSSP6).
XX
XX
XX Sequence 282 AA;
SQ
Query Match 100.0%; Score 1258; DB 21; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.4e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 GCEQRTTATESFPHPGFNNSLPNKDHNDIMLVKASPVSTWAVRPLTLLSRCTACTS 120
DB 114 GCEQRTTATESFPHPGFNNSLPNKDHNDIMLVKASPVSTWAVRPLTLLSRCTACTS 173
QY 121 CLISGSGTSSPOLRLPHTLRCAANTIIEHQKCNAYPGNITDTWVCASVOEGKDSGCG 180

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Db	174	CLISGWGSTSSPOLRLPHTLRCANITITIEHOKCENAYPGNITDTMVCASVQEGKDCOG	233
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Db	234	DSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN	282

Search completed: October 22, 2003, 15:51:34
Job time : 35.0587 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2003, 15:50:17 : Search time 21.9589 Seconds
(without alignments)
1746.375 Million cell updates/sec

Title: US-09-856-320A-2_COPY_54_282

Perfect score: 1258
Sequence: 1 IIKGFCKHSPQWALPE.....GYTVKCYVDMIQETMKNN 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	250	11	US-09-946-374-170 Sequence 170, App
2	1258	100.0	250	12	US-10-015-387A-170 Sequence 170, App
3	1258	100.0	250	12	US-10-137-870-506 Sequence 506, App
4	1258	100.0	250	12	US-10-140-018-506 Sequence 506, App
5	1258	100.0	250	12	US-10-140-021-506 Sequence 506, App
6	1258	100.0	250	12	US-10-140-274-506 Sequence 506, App
7	1258	100.0	250	12	US-10-140-471-506 Sequence 506, App
8	1258	100.0	250	12	US-10-140-807-506 Sequence 506, App
9	1258	100.0	250	12	US-10-140-922-506 Sequence 506, App
10	1258	100.0	250	12	US-10-140-924-506 Sequence 506, App
11	1258	100.0	250	12	US-10-140-926-506 Sequence 506, App
12	1258	100.0	250	12	US-10-141-698-506 Sequence 506, App
13	1258	100.0	250	12	US-10-141-702-506 Sequence 506, App
14	1258	100.0	250	12	US-10-141-704-506 Sequence 506, App
15	1258	100.0	250	12	US-10-142-421-506 Sequence 506, App

16	1258	100.0	250	12	US-10-142-432-506 Sequence 506, App
17	1258	100.0	250	12	US-10-142-767-506 Sequence 506, App
18	1258	100.0	250	12	US-10-143-033-506 Sequence 506, App
19	1258	100.0	250	12	US-10-144-994-506 Sequence 506, App
20	1258	100.0	250	12	US-10-145-628-506 Sequence 506, App
21	1258	100.0	250	12	US-10-145-631-506 Sequence 506, App
22	1258	100.0	250	12	US-10-145-633-506 Sequence 506, App
23	1258	100.0	250	12	US-10-145-746-506 Sequence 506, App
24	1258	100.0	250	12	US-10-145-748-506 Sequence 506, App
25	1258	100.0	250	12	US-10-145-823-506 Sequence 506, App
26	1258	100.0	250	12	US-10-145-826-506 Sequence 506, App
27	1258	100.0	250	12	US-10-145-870-506 Sequence 506, App
28	1258	100.0	250	12	US-10-145-876-506 Sequence 506, App
29	1258	100.0	250	12	US-10-145-959-506 Sequence 506, App
30	1258	100.0	250	12	US-10-146-724-506 Sequence 506, App
31	1258	100.0	250	12	US-10-146-725-506 Sequence 506, App
32	1258	100.0	250	12	US-10-146-795-506 Sequence 506, App
33	1258	100.0	250	12	US-10-147-495-506 Sequence 506, App
34	1258	100.0	250	12	US-10-147-501-506 Sequence 506, App
35	1258	100.0	250	12	US-10-147-504-506 Sequence 506, App
36	1258	100.0	250	12	US-10-147-506-506 Sequence 506, App
37	1258	100.0	250	12	US-10-147-509-506 Sequence 506, App
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45	1258	100.0	250	12	US-10-006-130A-170 Sequence 170, App

ALIGNMENTS

RESULT 1
US-09-946-374-170
Sequence 170, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PICI
CURRENT APPLICATION NUMBER: US/09/946,374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
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PRIOR FILING DATE: 1998-09-01
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PRIOR APPLICATION NUMBER: 60/105807

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DB 202 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVKCYVDWIOETMKN 250

RESULT 2
US-10-015-387A-170
Sequence 170, Application US/10015387A
Publication No. US20030135034A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth U.
APPLICANT: Pan, James
APPLICANT: Pan, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PIC54
CURRENT APPLICATION NUMBER: US/10/015,387A
CURRENT FILING DATE: 2001-12-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 170
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-10-015-387A-170

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DB 142 CLISGSGTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDITWVCASVOEGKDSGCG 201
QY 181 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVKCYVDWIOETMKN 229
DB 202 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVKCYVDWIOETMKN 250

RESULT 3
US-10-137-870-506
Sequence 506, Application US/10137870
Publication No. US20030138883A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330RIC155
CURRENT APPLICATION NUMBER: US/10/137,870
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-870-506

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Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 22 IIKGEFCKPHSQWQALFEKTRLLCGATLLIAPRWLLTAHCLKPRYIVHLGQHNLOKXE 81
QY 61 GGEQRTTATESFPHPGFNNSLPNKDRNDIMLVKASPVSIWAVRPLTLSSRCVTAGTS 120
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QY 121 CLISGSGTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDITWVCASVOEGKDSGCG 180
DB 142 CLISGSGTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDITWVCASVOEGKDSGCG 201
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Db      202 DSGGPLVNCNOSLQGIISWGDPCCATITRKPGVYTKVCKYVDWIOETMKN 250

RESULT 4
US-10-140-018-506
; Sequence 506, Application US/10140018
; Publication No. US20030138885A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-018-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIKGECKPHSQPMQALFEKTRLLCGATLTPRWLTAAHCLKRRIYVHGGHNLQKEE 60
Db      22 IIKGECKPHSQPMQALFEKTRLLCGATLTPRWLTAAHCLKRRIYVHGGHNLQKEE 81
QY      61 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 120
Db      82 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 141
QY      121 CLISWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVQEGKDCSCQG 180
Db      142 CLISWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVQEGKDCSCQG 201
QY      181 DSGGPLVNCNOSLQGIISWGDPCCATITRKPGVYTKVCKYVDWIOETMKN 229
Db      202 DSGGPLVNCNOSLQGIISWGDPCCATITRKPGVYTKVCKYVDWIOETMKN 250

RESULT 5
US-10-140-021-506
; Sequence 506, Application US/10140021
; Publication No. US20030138886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C161
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-021-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIKGECKPHSQPMQALFEKTRLLCGATLTPRWLTAAHCLKRRIYVHGGHNLQKEE 60
Db      22 IIKGECKPHSQPMQALFEKTRLLCGATLTPRWLTAAHCLKRRIYVHGGHNLQKEE 81
QY      61 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 120
Db      82 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 141
QY      121 CLISWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVQEGKDCSCQG 180
Db      142 CLISWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVQEGKDCSCQG 201
QY      181 DSGGPLVNCNOSLQGIISWGDPCCATITRKPGVYTKVCKYVDWIOETMKN 229
Db      202 DSGGPLVNCNOSLQGIISWGDPCCATITRKPGVYTKVCKYVDWIOETMKN 250

RESULT 6
US-10-140-274-506
; Sequence 506, Application US/10140274
; Publication No. US20030143674A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,274
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-274-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIKGECKPHSQPMQALFEKTRLLCGATLTPRWLTAAHCLKRRIYVHGGHNLQKEE 60
Db      22 IIKGECKPHSQPMQALFEKTRLLCGATLTPRWLTAAHCLKRRIYVHGGHNLQKEE 81
QY      61 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 120
Db      82 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 141
QY      121 CLISWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVQEGKDCSCQG 180
Db      142 CLISWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVQEGKDCSCQG 201
QY      181 DSGGPLVNCNOSLQGIISWGDPCCATITRKPGVYTKVCKYVDWIOETMKN 229
Db      202 DSGGPLVNCNOSLQGIISWGDPCCATITRKPGVYTKVCKYVDWIOETMKN 250
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-274-506

Query Match          100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECRPHSQPQWQALFEKTRLLCGATLIPRWMLTAAHCLKPRYIVHLCQHNLOKKE 60
DB 22 IIKGFECRPHSQPQWQALFEKTRLLCGATLIPRWMLTAAHCLKPRYIVHLCQHNLOKKE 81
QY 61 GCEQRTATSESPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 82 GCEQRTATSESPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
QY 121 CLISGSGTSSPOLRLPHTLRCAITIIEHOKCENAYPGNITDTWCASVQEGKDCSCG 180
DB 142 CLISGSGTSSPOLRLPHTLRCAITIIEHOKCENAYPGNITDTWCASVQEGKDCSCG 201
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVKCYVDWIOETMKN 229
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVKCYVDWIOETMKN 250

RESULT 7
US-10-140-471-506
; Sequence 506, Application US/10140471
; Publication No. US2003013887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-471-506

Query Match          100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECRPHSQPQWQALFEKTRLLCGATLIPRWMLTAAHCLKPRYIVHLCQHNLOKKE 60
DB 22 IIKGFECRPHSQPQWQALFEKTRLLCGATLIPRWMLTAAHCLKPRYIVHLCQHNLOKKE 81
QY 61 GCEQRTATSESPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 82 GCEQRTATSESPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
QY 121 CLISGSGTSSPOLRLPHTLRCAITIIEHOKCENAYPGNITDTWCASVQEGKDCSCG 180
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DB 142 CLISGSGTSSPOLRLPHTLRCAITIIEHOKCENAYPGNITDTWCASVQEGKDCSCG 201
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVKCYVDWIOETMKN 229
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVKCYVDWIOETMKN 250

RESULT 8
US-10-140-807-506
; Sequence 506, Application US/10140807
; Publication No. US2003013435A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-807-506

Query Match          100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECRPHSQPQWQALFEKTRLLCGATLIPRWMLTAAHCLKPRYIVHLCQHNLOKKE 60
DB 22 IIKGFECRPHSQPQWQALFEKTRLLCGATLIPRWMLTAAHCLKPRYIVHLCQHNLOKKE 81
QY 61 GCEQRTATSESPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 82 GCEQRTATSESPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
QY 121 CLISGSGTSSPOLRLPHTLRCAITIIEHOKCENAYPGNITDTWCASVQEGKDCSCG 180
DB 142 CLISGSGTSSPOLRLPHTLRCAITIIEHOKCENAYPGNITDTWCASVQEGKDCSCG 201
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVKCYVDWIOETMKN 229
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVKCYVDWIOETMKN 250

RESULT 9
US-10-140-922-506
; Sequence 506, Application US/10140922
; Publication No. US2003013889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
US-10-140-922-506
```

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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C179
; CURRENT APPLICATION NUMBER: US/10/140,922
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-922-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIKGFECKPHSQPQOALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHIGQHNLOKEE 60
    |||
DB 22 IIKGFECKPHSQPQOALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHIGQHNLOKEE 81
    |||
OY 61 GGEOTRTATESFPHGFNNSLPNKDHRNDIMLVKASPVSTTMAVRPLTSSRCVTAGTS 120
    |||
DB 82 GGEOTRTATESFPHGFNNSLPNKDHRNDIMLVKASPVSTTMAVRPLTSSRCVTAGTS 141
    |||
OY 121 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVQEGKDSGCG 180
    |||
DB 142 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVQEGKDSGCG 201
    |||
OY 181 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVKCYVDMIOETMKNN 229
    |||
DB 202 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVKCYVDMIOETMKNN 250
    |||

RESULT 10
US-10-140-924-506
; Sequence 506, Application US/10140924
; Publication No. US20030134355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C177
; CURRENT APPLICATION NUMBER: US/10/140,924
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-924-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIKGFECKPHSQPQOALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHIGQHNLOKEE 60
    |||
DB 22 IIKGFECKPHSQPQOALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHIGQHNLOKEE 81
    |||
OY 61 GGEOTRTATESFPHGFNNSLPNKDHRNDIMLVKASPVSTTMAVRPLTSSRCVTAGTS 120
    |||
DB 82 GGEOTRTATESFPHGFNNSLPNKDHRNDIMLVKASPVSTTMAVRPLTSSRCVTAGTS 141
    |||
OY 121 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVQEGKDSGCG 180
    |||
DB 142 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVQEGKDSGCG 201
    |||
OY 181 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVKCYVDMIOETMKNN 229
    |||
DB 202 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVKCYVDMIOETMKNN 250
    |||

RESULT 11
US-10-140-926-506
; Sequence 506, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C187
; CURRENT APPLICATION NUMBER: US/10/140,926
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-926-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIKGFECKPHSQPQOALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHIGQHNLOKEE 60
    |||
DB 22 IIKGFECKPHSQPQOALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHIGQHNLOKEE 81
    |||
OY 61 GGEOTRTATESFPHGFNNSLPNKDHRNDIMLVKASPVSTTMAVRPLTSSRCVTAGTS 120
    |||
DB 82 GGEOTRTATESFPHGFNNSLPNKDHRNDIMLVKASPVSTTMAVRPLTSSRCVTAGTS 141
    |||
OY 121 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVQEGKDSGCG 180
    |||
DB 142 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVQEGKDSGCG 201
    |||
OY 181 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVKCYVDMIOETMKNN 229
    |||
DB 202 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVKCYVDMIOETMKNN 250
    |||
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; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-924-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIKGFECKPHSQPQOALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHIGQHNLOKEE 60
    |||
DB 22 IIKGFECKPHSQPQOALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHIGQHNLOKEE 81
    |||
OY 61 GGEOTRTATESFPHGFNNSLPNKDHRNDIMLVKASPVSTTMAVRPLTSSRCVTAGTS 120
    |||
DB 82 GGEOTRTATESFPHGFNNSLPNKDHRNDIMLVKASPVSTTMAVRPLTSSRCVTAGTS 141
    |||
OY 121 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVQEGKDSGCG 180
    |||
DB 142 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVQEGKDSGCG 201
    |||
OY 181 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVKCYVDMIOETMKNN 229
    |||
DB 202 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVKCYVDMIOETMKNN 250
    |||

RESULT 11
US-10-140-926-506
; Sequence 506, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C187
; CURRENT APPLICATION NUMBER: US/10/140,926
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-926-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIKGFECKPHSQPQOALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHIGQHNLOKEE 60
    |||
DB 22 IIKGFECKPHSQPQOALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHIGQHNLOKEE 81
    |||
OY 61 GGEOTRTATESFPHGFNNSLPNKDHRNDIMLVKASPVSTTMAVRPLTSSRCVTAGTS 120
    |||
DB 82 GGEOTRTATESFPHGFNNSLPNKDHRNDIMLVKASPVSTTMAVRPLTSSRCVTAGTS 141
    |||
OY 121 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVQEGKDSGCG 180
    |||
DB 142 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVQEGKDSGCG 201
    |||
OY 181 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVKCYVDMIOETMKNN 229
    |||
DB 202 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVKCYVDMIOETMKNN 250
    |||
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QY	61	GGEORRTATESPPHGFENNSLPKHKHRNDIMVKASPSVITMAVPLTSSSCVAGTS	120
Db	82	GGEORRTATESPPHGFENNSLPKHKHRNDIMVKASPSVITMAVPLTSSSCVAGTS	141
QY	121	CLISMGSTSSPOLRPLPHTLRCAINTIIHOKECENAYPGNIPTDWCASVQEGSKDCOG	180
Db	142	CLISMGSTSSPOLRPLPHTLRCAINTIIHOKECENAYPGNIPTDWCASVQEGSKDCOG	201
QY	181	DSGGEPLVNCQSLQGIISWGDPCAIRRKPGVTVKVCYVDWIOETKKN	229
Db	202	DSGGEPLVNCQSLQGIISWGDPCAIRRKPGVTVKVCYVDWIOETKKN	250

RESULT 12
US-10-141

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? Sequence 506, Application US/10141698
? Publication No. US20030134357A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Beresini, Maureen
? APPLICANT: DeForge, Laura
? APPLICANT: Desnoyers, Luc
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerritsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Guiney, Austin L.
? APPLICANT: Sherwood, Steven
? APPLICANT: Smith, Victoria
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Watanabe, Colin K
? APPLICANT: Wood, William
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE OF INVENTION: ACIDS ENCODING THE SAME
? FILE REFERENCE: P330R1C206
? CURRENT APPLICATION NUMBER: US/10/141,698
? PRIORITY FILING DATE: 2002-05-08
? Prior Application removed - See Palm or File Wrapper
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 506
? LENGTH: 250
? TYPE: PRT
? ORGANISM: Homo Sapien
? US-10-141-698-506

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Query Match	100.0%	Score 1258	DB 12	Length 250
Best Local Similarity	100.0%	Pred. No. 14	118	
Matches 229	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	IIIGFECKPHSOQMOALFEKTRLLCGALLIPRMLLTAHCKRYVHIGHNLQKEE	60
Db	22 IIGFECKPHSOQMOALFEKTRLLCGALLIPRMLLTAHCKRYVHIGHNLQKEE	81
QY	61 GCEQRTATATESPFPHPFNNSLPNKHNDIMLVKASPVSLTMAVRPLTLSSRCVTAGTS	120
Db	82 GCEQRTATATESPFPHPFNNSLPNKHNDIMLVKASPVSLTMAVRPLTLSSRCVTAGTS	141
QY	121 CLISMGSTSSPOLRLPHTLRLRCANTITIEHOKENAYPGNITDPMVCASVQEGKDSQCG	180
Db	142 CLISMGSTSSPOLRLPHTLRLRCANTITIEHOKENAYPGNITDPMVCASVQEGKDSQCG	201
QY	181 DSGGRLVNCOSLOGIISWGMDPCATLRKRGVYTKYCKYVDMIOETMKKN	229
Db	202 DSGGRLVNCOSLOGIISWGMDPCATLRKRGVYTKYCKYVDMIOETMKKN	250

RESULT 13
US-10-141-702-506
; Sequence 506, Application US/10141702
; Publication No. US20030134358A1

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: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P330R1C208
: CURRENT APPLICATION NUMBER: US/10/141,702
: CURRENT FILING DATE: 2002-05-08
: Prior Application removed - See Palm or File Wrapper
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 506
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Homo Sapien
: OS-10-141-702-506

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Query Match	100.0%	Score 1258	DB 12	length 250
Best Local Similarity	100.0%	Pred. No. 14e-118		
Matches 229	Conservative 0	Mismatches 0	Indels 0	Gaps 0

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Db	22	IIKGFCKRHSQPMQAALEKTRLLICGATLLAPRWLLTAAHCLEKRYIVHGHQNNLOKEE	81
QY	61	GCEQRTATSESPHPEGFNLSLPNKDHRDMLVVKASFSVITMAVRBELTSSRCVTAGTS	120
Db	82	GCEQRTATSESPHPEGFNLSLPNKDHRDMLVVKASFSVITMAVRBELTSSRCVTAGTS	141
QY	121	CLISGSGTSSPOLRLPHTLRCAINTIIIEHCKCENAAVPGNITDTMVCASVOEGGKSCQG	180
Db	142	CLISGSGTSSPOLRLPHTLRCAINTIIIEHCKCENAAVPGNITDTMVCASVOEGGKSCQG	201
QY	181	DSGGPLVNCNOSLQGIISMGDPCATTRKEGYTVVCYVVMIOETMKN	229
Db	202	DSGGPLVNCNOSLQGIISMGDPCATTRKEGYTVVCYVVMIOETMKN	250

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US-RESULT 4
US-10-141-704-506
Sequence 506, Application US/10141704
Publication No. US20030134359A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Flivaloff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Andrew
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunnas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William

```

```

; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C209
; CURRENT APPLICATION NUMBER: US/10/141,704
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-704-506

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```

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 IIKFECKPHSQPWOAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
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   |||
QY 61 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGTS 120
   |||
Db 82 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGTS 141
   |||
QY 121 CLISGWSSTSPQLRLPHTLRCAANTIIIEHOKCENAYPGNITDTMVCAVQEGGKDSGCG 180
   |||
Db 142 CLISGWSSTSPQLRLPHTLRCAANTIIIEHOKCENAYPGNITDTMVCAVQEGGKDSGCG 201
   |||
QY 181 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNK 229
   |||
Db 202 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNK 250
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RESULT 15
US-10-142-421-506
; Sequence 506, Application US/10142421
; Publication No. US20030134360A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C218
; CURRENT APPLICATION NUMBER: US/10/142,421
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-421-506

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Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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   |||
Db 22 IIKFECKPHSQPWOAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
   |||
QY 61 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGTS 120
   |||
Db 82 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGTS 141
   |||
QY 121 CLISGWSSTSPQLRLPHTLRCAANTIIIEHOKCENAYPGNITDTMVCAVQEGGKDSGCG 180
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Db 142 CLISGWSSTSPQLRLPHTLRCAANTIIIEHOKCENAYPGNITDTMVCAVQEGGKDSGCG 201
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QY 181 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNK 229
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 14:08:00 ; Search time 3410.8 seconds
(without alignments)
2746.659 Million cell updates/sec

Title: US-09-856-320a-2_COPY_54_282
Perfect score: 1258
Sequence: 1 IIRKFECKRHSQPMQALPE.....GVYTKVCKYVDVIQETMKNN 229

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 2888711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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17: em_hum.*
18: em_in.*
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20: em_om.*
21: em_or.*
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23: em_pat.*
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41: em_hcg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1258	100.0	1106	6	AX016287 Sequence
2	1258	100.0	1106	6	BD137019 Human CAS
3	1258	100.0	1158	6	AX016289 Sequence
4	1258	100.0	1158	6	BD137020 Human CAS
5	1258	100.0	1181	6	AB013730 Homo sapi
6	1258	100.0	1186	9	AB012917 Homo sapi
7	1258	100.0	1192	6	AR152174 Sequence
8	1258	100.0	1204	6	AX358932 Sequence
9	1258	100.0	1204	6	AX362425 Sequence
10	1258	100.0	1204	6	AX454622 Sequence
11	1258	100.0	1204	6	AX464372 Sequence
12	1258	100.0	1204	6	AX491100 Sequence
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14	1258	100.0	1213	6	BC022068 Homo sapi
15	1258	100.0	1301	6	BD091587 Novel ser
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23	1219.5	96.9	1052	6	AR219287 Sequence
24	1213	96.4	833	6	AR060847 Sequence
25	1213	96.4	833	6	BD082136 Novel pro
26	1062	84.4	1213	10	AB016226
27	1062	84.4	1256	6	AB016227
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29	1014.5	80.6	1164	6	AX661915 Sequence
30	956	76.0	9120	9	AF164623 Homo sapi
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36	897.5	71.3	200792	2	AC140096 Pan trogl
37	885.5	70.4	176647	2	AC130782 Sequence
38	782.5	62.2	226890	2	AC130188 Papio anu
39	782.5	62.2	228413	2	AC135541 Rattus no
40	782.5	62.2	243655	2	AC127853 Rattus no
41	687.5	54.6	974	10	AC099172 Rattus no
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45	684	54.4	1333	6	D30785 Mouse mRNA
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RESULT 1

ALIGNMENTS

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LOCUS AX016287 1106 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from Patent WO949055.
ACCESSION AX016287
VERSION AX016287.1 GI:10041854
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.
Human casb12 polypeptide, a serine protease
Patent: WO 949055-A 1 30-SEP-1999;
JOURNAL BRUCK CLAUDE ELVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);
COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA
(BE)
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source location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 247 a 348 c 287 g 224 t
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Alignment Scores:
Pred. No.: 4.14e-97 Length: 1106
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
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QY 21 lylthrtargleuleucysglvalathrleuilealaproargtrpleuethrilaala 40
DB 233 AAGACGGGCTACTCTGTGGGGCGAGCGCTCATCGCCCGCAGATGGCTCTGACACAGCC 292
QY 41 hiscysleuylsproargtrylevalhisleuglyglnhisasnleuglnlysglu 60
DB 293 CACTGCTCAAGCCCGGCTACATAGTTCACTCGGGGCGACACACCTCCAGAGGAGG 352
QY 61 glycysgluglnthrtargthralthrghuserpheprohisserglnpheasnser 80
DB 353 GGCTGTGACAGACCCGGACAGCCAGCTGCTCTCCACCCCGGCTTCAACACAGC 412
QY 81 leuproasnlyasphsarsasnspilemetleuvallysmetalaserprovalser 100
DB 413 CTCCTCAACAAAGACCCGCAATGACATCATGCTGGTGAAGATGGCATCCGCACTCC 472
QY 101 llethrtpralaalaargproleuthrleuserserargcysvalthrilaaglythrser 120
DB 473 ATCACTGGGCTGTGCGACCCCTCACTCTCTCACTGCTGCTGCTGCGACAGC 532
QY 121 cysleuileserglvtrogllyserthrserserproglinleuargleuprohisthrleu 140
DB 533 TGCTCTATTTCCGGCTGGGGGCGACAGCTCCAGCCCTTACGCTGCTTACACCTTG 592
QY 141 argcysalaasnlethrillelleglnhisglnlyscysgluasnalaatyrrproglyasn 160
DB 593 CGATCGGCAACATACCATCATTTAGAGCACAGAAAGTGTGAAGAGCCGCGGCAAC 652
QY 161 llethrtaspthmetvalcysalaservalingluelylyaspserserysglnly 180
DB 653 ATCAAGACACCATGTGTGTGCTGCGAGCGTGCAGAGGGGCGCAAGACTCCGCGAGGT 712
QY 181 aspsersgylglyprleuvalcysasnnglnserleuglnlyllellesertrpglygn 200

DB 713 GACTCCGGGGCCCTCTGTGTGTACCAAGTCTTCAAGCATTTCTCGGGGCCAG 772
QY 201 asprocysalaaliethrarglysrprogllyvaltyrthrlyvalcyslystyrrvalasp 220
DB 773 GATCCGTGTGGATCACCCGAAAGCTGTGTCTACAGAAAGTGTCAATATGTGAC 832
QY 221 trpilleglnuthrmetlyasnasn 229
DB 833 TGGATCCAGAGAGCATGAAGAACAAAT 859
RESULT 2
LOCUS BD1337019 1106 bp DNA linear PAT 18-SEP-2002
DEFINITION Human CASB 12 polypeptide, a serine protease.
ACCESSION BD1337019
VERSION BD1337019.1 GI:23231964
KEYWORDS JP 2002507425-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1106)
Bruck,C.E.M., Cassart,J.P., Coche,T. and Bassols,C.V.
Human CASB 12 polypeptide, a serine protease
Patent: JP 2002507425-A 1 12-MAR-2002;
JOURNAL SMITHKLINE BEECHAM BIOLOGICALS SA
COMMENT
OS Homo sapiens (human)
PN JP 2002507425-A/1
PF 12-MAR-2002
PD 17-MAR-1999 JP 2000538015
PR 20-MAR-1998 GB 9806095.7
PI CLAUDE ELVIRE MARIE BRUCK,JEAN POL CASSART, THIERRY COCHE, PI
CARLOTA VINALS BASSOLS
PC C12N15/09,A61K31/70,A61K38/00,A61P35/00,A61P37/02,C07K16/40,
PC C12N15/15,
PC C12N1/19,C12N1/21,C12N5/10,C12N9/64,C12P21/02,C12Q1/02,C12Q1/15,
PC 68,G01N33/15,
PC G01N33/50,G01N33/50,G01N33/574,G01N33/68,C12N15/00,A61K37/02,
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CC Human CASB 12 polypeptide, a serine protease. FH Key
Location/Qualifiers
FT source 1..1106
/organism="Homo sapiens (human)".
FEATURES
source location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 247 a 348 c 287 g 224 t
ORIGIN
Alignment Scores:
Pred. No.: 4.14e-97 Length: 1106
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-856-320A-2_COPY_54_282 (1-229) x BD1337019 (1-1106)
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DB 173 ATCATCAAGGGGTTGAGTGCAGAGCTTCACTCCAGCCCTGGCAGGACCTGTTCCAG 232
QY 21 lylthrtargleuleucysglvalathrleuilealaproargtrpleuethrilaala 40
DB 233 AAGACGGGCTACTCTGTGGGGCGACCGCTCATCGCCCGCAATGGCTCTGACAGCAGCC 292
QY 41 hiscysleuylsproargtrylevalhisleuglyglnhisasnleuglnlysglu 60
DB 293 CACTGCTCAAGCCCGGCTACATAGTTCACTCGGGGCGACACACCTCCAGAGGAGG 352

QY 61 GlyCyseGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
DB 353 GCGTGTGAGAGACCGGAGCAGCCATCGAGTCTTCCCCACCCGGCTTCACACAGC 412
QY 81 LeuProAsnLysAspHisAspAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 413 CTCCTCAACAAACACCGCAATGATCATCTGTGTAAGATGGCATGCGACGCTCC 472
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrIleGlyThrSer 120
DB 473 ATACCTGGGCTGTGGAGCCCTCACCCTCTCTCTACGCTGTGTCTACTGTGGACACAGC 532
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 533 TGGCTCATTTCCGGCTGGGGGACACGTCAGCCGCCAGTTAGCCGCTTCACACTTG 592
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
DB 593 CGATGGCCAAACATCACCATCATTTAGACACAGAGGTGAGAAAGCCCTACCCGGCAAC 652
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180
DB 653 ATACAGACACCATGGTGTGTGTCAGGTCAGAGGAGGGGCAAGGACTCTGGCCAGGT 712
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB 713 GACTCCGGGGGCGCTGTGTCTGTACACAGTCTCTTCAAGGCTTATCTCTGGGGCCAG 772
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
DB 773 GATCCCTGTGGCATACCCGAAAGCCTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC 832
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
DB 833 TGGATCCAGAGACGATGAGAACAAAT 859

RESULT 3
AX016289 1158 bp DNA linear PART 07-SEP-2000
LOCUS AX016289
DEFINITION Sequence 3 from Patent WO949055.
ACCESSION AX016289
VERSION AX016289.1 GI:10041855
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 Bruck, C.E., Coche, T., Caessart, J.P. and Vinals-Bassols, C.
AUTHORS Human casb12 polypeptide, a serine protease
TITLE Patent: WO 94/9055-A 3 10-SEP-1999.
JOURNAL BRUCK CLAUDINE ELVIRE MARIE (BE); SMITHKLINE BECHAM BIOLOG (BE);
COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTTA
(BE)

FEATURES
source 1..1158
Location/Qualifiers
1..1158
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 274 a 359 c 306 g 219 t
ORIGIN

Alignment Scores:
Pred. No.: 4 35e-97 Length: 1158
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x AX016289 (1-1158)
QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaIleLeuPheGlu 20

DB 243 ATCATCAAGGGGTTCAGTGAAGCAAGCTCTACCTCCAGCCTTGGAGGACCCCTGTCGAG 302
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40
DB 303 AAGACCGGCTACTCTGTGGGGGAGCGCTCATTCGCCCCAGATGGCTCTGTACAGCAGCC 362
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
DB 363 CACTGCTCAAGCCCGCTTACATAGTTACCTGGGGACACACACTTCAGAAAGAGAG 422
QY 61 GlyCyseGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
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DB 603 TGGCTCATTTCCGGCTGGGGGACACGTCAGCCGCCAGTTAGCCGCTTCACACTTG 662
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
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QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
DB 903 TGGATCCAGAGACGATGAGAACAAAT 929

RESULT 4
BD137020 1158 bp DNA linear PART 18-SEP-2002
LOCUS BD137020
DEFINITION Human CASB 12 polypeptide, a serine protease.
ACCESSION BD137020
VERSION BD137020.1 GI:23231965
KEYWORDS JP 2002507425-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 (bases 1 to 1158)
AUTHORS Bruck, C.E.M., Caessart, J.P., Coche, T. and Bassols, C.V.
TITLE Human CASB 12 polypeptide, a serine protease
JOURNAL Patent: JP 2002507425-A 2 12-MAR-2002;
SMITHKLINE BECHAM BIOLOGICALS SA

COMMENT
OS Homo sapiens (human)
PN JP 2002507425-A/2
PD 12-MAR-2002
PF 17-MAR-1999 JP 2000538015
PR 20-MAR-1998 GB 9806095.7
PI CLAUDINE ELVIRE MARIE BRUCK, JEAN POL CASSART, THIERRY COCHE, PI
CARLOTTA VINALS BASSOLS
PC C12N15/09, A61K31/70, A61K38/00, A61P35/00, A61P37/02, C07K16/40,
C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12N9/64, C12P21/02, C12Q1/02, C12Q1/

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PC 68.G01N33/15
PC G01N33/50,G01N33/50,G01N33/574,G01N33/68,C12N15/00,A61K37/02,
PC C12N5/00
CC Human CASB 12 polypeptide, a serine protease. FH Key
Location/Qualifiers
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Alignment Scores:
Pred. No.: 4.35e-97 Length: 1158
Score: 1258.00 Matches: 229
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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DB 303 AAGAGCGGGCTTCTCTGGGGCGAGCTCATGCCCCAGATGGCTCTTGACAGCAGCC 362
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
DB 363 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAGAGAG 422
QY 61 GlyCySGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80
DB 422 GGCTGTGACGACCCGGCAGCCAGCTAGTCTTCCCGCCAGCCCGGCTTCAACAACGC 482
QY 81 LeuProAsnLysASPHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 483 CTCCTCCACAAAGACCCGCAATGATCATGCTGGTGAAGATGGCATGCCAGTCTCC 542
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 543 ATCACCCTGGGCTGTGGACCCCTCAACCTCTCCTCAGCGTGTGTCACGTCTGGACACGC 602
QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
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QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
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QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysIleSerTrpValAsp 220
DB 843 GATCGGTGGCATACCCGAAAGCTGTGTCTTACAGAAAGTCTGCATAATATGTGAC 902
QY 221 TrpIleGlnGluThrMetLysAsnSer 229
DB 903 TGGATCCAGAGACGATGAAGAAAT 929

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RESULT 5
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LOCUS AB013730 1181 bp mRNA linear PRI 20-JUN-2000
DEFINITION Homo sapiens mRNA for Hippostasin, complete cds.
ACCESSION AB013730
VERSION AB013730.1 GI:6681453
KEYWORDS Hippostasin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (sites)
REFERENCE
AUTHORS Mitsui,S., Yamada,T., Okui,A., Komimami,K., Uemura,H. and
Yamaguchi,N.
TITLE A novel isoform of a kallikrein-like protease, TUSP/hippostasin,
(JPRS20), is expressed in the human brain and prostate
Biochem. Biophys. Res. Commun. 272 (1), 205-211 (2000)
JOURNAL PubMed 10872828
2 (bases 1 to 1181)
Yamaguchi,N. and Mitsui,S.
AUTHORS Direct Submission
TITLE Submitted (08-MAY-1998) Nozomi Yamaguchi, Kyoto Prefectural
University of Medicine, Res. Ins. Geriatrics; Kawarimachi Hirokoji,
Kyoto, Kyoto 602-8566, Japan (E-mail:nozomi@koto.kpu-m.ac.jp,
Tel:81-75-251-5848, Fax:81-75-251-5848)
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DB: 9 Gaps: 0
US-09-856-320A-2_COPY_54_282 (1-229) x AB013730 (1-1181)
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DB 244 AAGAGCGGGGTTCTCTGGGGCGAGCTATGCCCGCCAGATGGCTCTGACAGCAGCC 303
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
DB 304 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAGAGAGAG 363
QY 61 GlyCySGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80
DB 364 GGCTGTGACGACCCGAGCAGCAGCTAGTCTTCCCGCCAGCCCGGCTTCAACAACAGC 423

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OY	81	IeuProAsnLysASPHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer	100
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OY	101	IleThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer	120
Db	484	ATCACCTGGGCTGTGGAGCCCTCAACCCCTCTCTCCTACGCTGTGATCTGTGGACACAG	543
OY	121	CysLeuIleSerGlyThrGlySerThrSerSerProGlnLeuAlaGlyLeuProHisThrLeu	140
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Db	604	CGATCGGCCCAATATACCATTCATTAGACACCAAGATGGAGAACGCCCTTACCCCGGAAAC	663
OY	161	IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly	180
Db	664	ATCACAGACACCATGATGTGTGCCAGCGTCAGGAAGGGGGCAAGGACTCCGCCAGGGGT	723
OY	181	AspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyTleIleSerThrProGlyGln	200
Db	724	GACTCCGGGGGCCCCCTGTGCTGTGTATCCAGTCTCTTCAAGGGATTAATCTCCCTGGGGCCAG	783
OY	201	AspProCysAlaIleThrArgLysProGlyValIlyrThrLysValCysLysTyrValAsp	220
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DEFINITION	Homo sapiens mRNA for serine protease (TLSP), complete cds.			
ACCESSION	AB012917			
VERSION	AB012917.1	GI:3649790		
KEYWORDS	TLSP; serine protease (TLSP).			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1			
AUTHORS	Yoshida,S., Taniguchi,M., Suemoto,T., Oka,T., He,X. and Shiosaka,S.			
TITLE	cDNA cloning and expression of a novel serine protease, TLSP			
JOURNAL	Biochim. Biophys. Acta 1399 (2-3), 225-228 (1998)			
MEDLINE	98438738			
PUBMED	9765601			
REFERENCE	2 (bases 1 to 1186)			
AUTHORS	Yoshida,S.			
TITLE	Direct Submission			
JOURNAL	Submitted (10-Apr-1998) Shigeraka Yoshida, Department of Anatomy 1, Asahikawa Medical College; Midorigacka Higashi 2-1-1, Asahikawa, Hokkaido 078-8510, Japan [E-mail:syoshiada@asahikawa-med.ac.jp, Tel.:81-166-66-2300, Fax:81-166-66-2309]			

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CDS	26. .874

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US-09-856-320A-2_COPY_54_282 (1-229) X AB012917 (1-1186)

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Oy		21	LysThrArIgleuleuCySGilyAlathrIleulleaIaProArgTrpleuLeuthralala	40
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Oy		61	GlyCySgluglInthrArgrThAlaThicIuSerPheProHisProGlyPheasnaBnsEr	80
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Oy		81	LeuProAsnuLysAphIsarAsnaAspiIemelleuValIysMetAlaserProvaliser	100
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DEFINITION	Sequence 8 from patent US 6232456.			PAT 08-AUG-2001
ACCESSION	ARI52174			
VERSION	ARI52174.1 GI:15118224			
KEYWORDS	Unknown.			

ORGANISM Unknown.
Unclassified.
1 (bases 1 to 1192)
REFERENCE Cohen,M., Colpitts,T.L., Friedman,P.N., Granados,E., Klaes,M.R.,
AUTHORS Russel,J.C., Stewart,K.D. and Stroppe,S.D.
TITLE Serine protease reagents and methods useful for detecting and
treating diseases of the prostate
JOURNAL Patent: US 6232456-A 8 15-MAY-2001;
FEATURES Location/Qualifiers
source 1..1192
BASE COUNT 279 a 385 c 280 g 238 t
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Pred. No.: 4,48e-97 Length: 1192
Score: 1258.00 Matches: 229
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Query Match: 100.00% Indels: 0
DB: Gaps: 0
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DB 230 AAGAGCGGCTACTCTGTGGGCGAGGCTCATCGCCCAAGTGGCTCTTGACAGCAGCC 289
QY 41 HisCySLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
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DB 650 ATCACAGACACCATGTGTGTGCGACGTCGAGAAAGGGGCGAGAGACTCCGCCAGGGT 709
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AX358932
LOCUS AX358932 1204 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 185 from Patent WO0193983.
ACCESSION AX358932
VERSION AX358932.1 GI:18675367
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Baker,K.P., Desnoyers,L., Gerlisen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 185 13-DEC-2001;
FEATURES Genentech Inc. (US)
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Best Local Similarity: 100.00% Mismatches: 0
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US-09-856-320A-2_COPY_54_282 (1-229) x AX358932 (1-1204)
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QY 21 lysThrArgLeuLeuCySGlYAlaThrLeuileAlaProArgTPLeuLeuThrAla 40
DB 229 AAGAGCGGCTACTCTGTGGGCGAGGCTCATCGCCCAAGTGGCTCTTGACAGCAGCC 288
QY 41 HisCySLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
DB 289 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGCAGCACACCTCCAGAAAGAGAGAG 348
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DB 349 GGCTGTGAGCAGACCCGAGCAGCCACTGACTCTTCCCGCCAGCTTCAACACAGC 408
QY 81 LeuProAsnLysASPHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 409 CTCGCCAACAAGACACCGCAATGACATCATCTGTGTAAGATGGCATCGCAGTCTCC 468
QY 101 lleThrTPAlaValArgProLeuThrLeuSerSerArgCyValThrAlaGlyThrSer 120
DB 469 ATCACTGGGCTGTGCGACCCCTCAACCTCTCTCACTGTGCTGCTGGCAGCAGC 528
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DB 529 TGCCCTATTTCGGGCTGGGGCAGCAGTCCAGCCCCCAGTTACGCTGCTTACACCTTG 588
QY 141 ArgCySAlaAsnIleThrIleIleGlnHisGlnLysCySGlUAsnAlaTyrProGlyAsn 160
DB 589 CGATCGCCCAACATCATCATCTATTGAGCACCAGAAAGTGTGAGAAAGCCTTACCCGGCAGC 648
QY 161 lleThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSerCySGlnGly 180
DB 649 ATCACAGACACCATGTGTGTGCGACGTCGAGAAAGGGGCGAGAGACTCCGCCAGGGT 708
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTPGlyGln 200

Db 709 GACTCCGGGGCCCTGCTCTGTAACCACTCTCTCAAGCATTTATCTCTGGGGCAG 768
QY 201 AASPProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
Db 769 GATCCCTGTGGCATCACCCGAAAGCCGTGGTCTACAGAAAGTTCGAAATATGTGAC 828
QY 221 TPTlGlnGluThrMetLysAsnAsn 229
Db 829 TGGATCCAGAGACGATGAAGAACAT 855
RESULT 9
AX362425 1204 bp DNA linear PAT 15-FEB-2002
LOCUS Sequence 185 from Patent WO0208288.
DEFINITION AX362425
ACCESSION AX362425
VERSION AX362425.1 GI:18694670
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 185 31-JAN-2002;
Genentech, Inc. (US)
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BASE COUNT 306 a 364 c 294 g 240 t
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Pred. No.: 4.53e-97 Length: 1204
Score: 1258.00 Matches: 229
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Best Local Similarity: 100.00% Mismatches: 0
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QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrLeuLeuThrAlaAla 40
Db 229 AAGACGGCGCTACTGTGGGGGAGCGCTCATCGCCGCCAGATGGCTTCGACAGAGCC 288
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
Db 289 CACTGCTCTCAAGCCCGCTACATAGTTCACTGGGGCAGACACACCTCCAGAGGAGGAG 348
QY 61 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80
Db 349 GCGTGTGACGACACCCGACACCCAGCTGCTCTCCACCCCGGCTTCAACACACAC 408
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 409 CTCGCCCAACAAAGACACCGCAATGATCATGTGTGAAGATGATGCGCAGCTCC 468
QY 101 IleThrTyrAlaValArgProLeuThrLysSerSerArgCysValThrAlaGlyThrSer 120
Db 469 ATCACTGGGCTGTGGACCCCTCACTCTCTCAACGCTGTGTCACTGCTGGACACAGC 528
QY 121 CysLeuIleSerGlyTyrPlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140

Db 529 TGGCTATTTCGGGCTGGGGGAGACAGTCCAGCCCACTTACGCTGCTACACACTTG 588
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Db 589 CATGCGCCAAATCATCCATATTGAGACACAGAGTGTGAGAACCCCTACCCCGGCAAC 648
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QY 181 AASPserGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTTPGlyGln 200
Db 709 GACTCCGGGGCCCTGCTGCTGTAACCACTCTCTCAAGCATTTATCTCTGGGGCAG 768
QY 201 AASPProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
Db 769 GATCCGTGTGCATCACCCGAAAGCCGTGGTCTACAGAAAGTTCGAAATATGTGAC 828
QY 221 TPTlGlnGluThrMetLysAsnAsn 229
Db 829 TGGATCCAGAGACGATGAAGAACAT 855
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LOCUS Sequence 207 from Patent WO0208284.
DEFINITION AX454622
ACCESSION AX454622
VERSION AX454622.1 GI:21713935
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.I.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 207 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 306 a 364 c 294 g 240 t
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Alignment Scores:
Pred. No.: 4.53e-97 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Db	229	AAGAGCGGGCTACTCTGTGAGGGGCGAGCGCTCANTGGCCCCAGATGAGTCTCTGTGACAGACGC	288
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Db	289	CACCTGCTTCAAGCCCCCGCTACCTAGATTCCACTCGGGGAGACAACTCCAGAAAGAGAG	348
OY	61	GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnSer	80
Db	349	GGCTGTGAGCAGACCCGGAGCAGCCACTGAGTCTTCCCCACCCGGCTTCAACAACAGC	408
OY	81	LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer	100
Db	499	CTCCCCAACAAGACACCCGCAATGACATCATGCTGCTGATGATGATGGCATCGCACTTCC	468
OY	101	IleThrTyrPalaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer	120
Db	469	ATCACCTGGGCTGTGCGACCCCTCACTCTCTCAAGCTGTGTGCTACGTGGACACAGC	528
OY	121	CysLeuIleSerGlyTyrGlySerThrSerSerProGlnIleArgLeuProHisThrLeu	140
Db	529	TGCTTCATTTCCGGCTGGGGGAGCAGCTCCACCCCAAGTTAGGCTGCTGCTACACTTG	588
OY	141	ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsn	160
Db	589	CGATCGGCCACATCATCATTATGACACCAAGAGTGTGAGAAAGCCTTACCCCGGCAAC	648
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Db	649	ATCACAGACACCATGTGTGTGCCAGCGAGGAAGGGGGGCAAGAGCATCTCGCCAGGTT	708
OY	181	AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGln	200
Db	709	GACTCGGGGGGCCCTGTGCTGTGAACAGTCTCTTCAAGCATTAATCTCCGGGGCCAG	768
OY	201	AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysIleTyrValAsp	220
Db	769	GATCCGTGTGCATATACCCGAAAGCCTGTGTCTTACAGAAAGTCTCGAAATATGTGGAC	828
OY	221	TyrIleGlnGluThrMetLysAsnAsn	229
Db	829	TGGATCCAGAGACGATGAAGAACAAT	855
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LOCUS			
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ACCESSION	AX464372		
VERSION	AX464372.1		
KEYWORDS	GI:21899202		
SOURCE			
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE			
AUTHORS	1 Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,		
	Gao, W.-Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,		
	Shenwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,		
	Wood, W.L. and Zhang, Z.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding		
JOURNAL	Name		
FEATURES	Patent: WO 0140466-A 505 07-JUN-2001;		
source	Genentech Inc. (US)		
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QY	21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla	40	
Db	229 AAGACGGGGCTACTCTGTGGGGCGAGCCTCATTCGCCCCCAATGAGCTCTGACAGCAGCC	288	
QY	41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu	60	
Db	289 CACTGCTCCAAAGCCCGCTACATGATGTTCACTGGGGGCGAGCAACCTCCAGAGAGAG	348	
QY	61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer	80	
Db	349 GGCTGTGAGCAGACCCCGACAGCCACGTAGCTCTTCCCAACCCCGCTTAAACAACAGC	408	
QY	81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer	100	
Db	409 CTCCCAACAAGACACCCGCAATGACATCATGCTGTGAAGATGGCATCGCCAGTCTCC	468	
QY	101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer	120	
Db	469 ATCACTGGCGTGTGGCAGCCCTCACCTCTCTCAAGCTGTGTACATGCTGGACCGC	528	
QY	121 CysLeuLysSerGlyTrpGlySerThrSerSerProGlnLeuAlaGluProHisThrLeu	140	
Db	529 TGCCCTCATTTCCGGCTGGGGCGAGCAGCTCCAGCCCCCGATTACCGCTCCCTCACACCTTG	588	
QY	141 ArgCysAlaAsnIleThrIleGlnHisGlnLysCysGluAsnAlaTyProGlyAsn	160	
Db	589 CGATGCGCAATCACCATCATATTGAGACCCAGAAAGTGTGAACGCTTACCCCGGCAAC	648	
QY	161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly	180	
Db	649 ATCAGACAGACCATGTGTGTGTGTGCCAGCTGACGAAAGGGGCAAGACTCTCCGACAGGT	708	
QY	181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln	200	
Db	709 GACTCCGGGGCCCTCTGTGCTGTGAACAGACTCTTCAAGGCATTATCTCTGGGGCCAG	768	
QY	201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyValAsp	220	
Db	769 GATCCGTGTGGATCACCCGGAAGCTGTGTCTTACACGAAAGTCTGCAATATGTGGAC	828	
QY	221 TrpIleGlnGlnThrMetLysAsnAsn	229	
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DEFINITION	Sequence 207 from Patent WO0200690.		
ACCESSION	AX491100		
VERSION	AX491100.1	GI:22323887	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 Baker, K.P., Ferrara, N., Garber, H., Gerritsen, M.E., Goddard, A.,		
	Godowski, P.J., Gurney, A.L., Hillan, K.J., Masters, S.A., Pan, J.,		
	Pao, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.		
	and Ye, W.		
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angioedem		

Qy	201	AspProCysAlaIleThrArguysProGlyValTyrThrLysValCysLysGlyTyrAlaAsp	220
Db	769	GATCCGTGTGGCATCAACCCGAAAGCCTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC	828
Qy	221	TrpIleGlnGluTyrMetLysAsnAsn	229
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DEFINITION	Homo sapiens, kallikrein 11, clone MGC:33060 IMAGE:4824387, mRNA,		
ACCESSION	BC022068		
VERSION	BC022068.1		
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
REFERENCE	1 (bases 1 to 1213)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshitsuki and Piero Carninci (RIKEN) cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadams@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting		
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OY	21	LysThrArgLeuLeuCysGIYAIAeThrLeuIleaIProAgTrPLeuLeuThraIaIa	40	
Dd	256	AAGACGGGGACTCTGTGGGGCCACGCTCATGCCCCCAGATGGCTCTCACAGCACC	315	
OY	41	HisCysLeuIysProArGlyrIleValHisLeuGIglnHisAsnLeuGInLysGIuGu	60	
Dd	316	CACGCGCTCAAGCCCCGGCTACATAGTTCCACTGGGGAGCACAACCTCCAGAAGAGAG	375	
OY	61	GIyCSgluGlnInThraGThraIaThnglUserTheProHISProGlyPhasAnaSnsr	80	
Dd	376	GGCTGTGAGCAGACCGGACGACCCAGTCCCTTCCCCACCCGGCTTCAACAACAGC	435	
OY	81	LeuProAsnLysASPHISARGASnaSPILemeteuValLysMecAlaSerProValse	100	
Dd	436	CTCCCCAACAAAGACACCCGCAATGACATCATCTGCTGAAGATGGCATGCCAGTCTCC	495	
OY	101	IleThrTPalavaIaArgProLeuThrLeuSerSerArgCysValThraIGlyThrsr	120	
Dd	496	ATCACCTGGGGCTGTGGCAGCCCTCACCTCTCTCACGCTGTGCATGCTGGCACAGC	555	
OY	121	CysLeuIleserGIYTPrpGlySerThrsSerProGlnLeuArgLeuProHisThrIeu	140	
Dd	556	TGCCTCATTTCCGGCTGGGGAGGACGCTCACGCCCCAGATTACGCTGCTCACACCTTG	615	
OY	141	ArgCysAlaAsnIleThrIleIleGIuHISGInLysCysGIuAsnaIaTYrProGIVasn	160	
Dd	616	CGATGGCCCAACATCATCACCATTATTGAGCACCAAGATGTGAAGACGCTTACCCGGCACC	675	
OY	161	IleThrASPThrMeValCysAlaSerValGInguIyGIyLysaspSerCysGIuGIy	180	
Dd	676	ATCACAGACACCATGAGTGTGTGCCAGCGTGCAGAAAGGGGCAAGGACTCTGCCAGAGGT	735	
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Dd	796	GATCCGAGTGGATCACCCGAAACCTCGGTGTCTTACAGAAAGTGTGCATAATATGTGCAC	855	
OY	221	TriPlegInGUthrMetLysAsnAsn	229	
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DEFINITION	Novel serine protease BSSP6.			
ACCESSION	BD091587			
VERSION	BD091587.1	GI:22637198		
KEYWORDS	WO 0031257-A/1.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
JOURNAL	Uemura,H., Okui,A., Kominami,K., Yamaguchi,N. and Mitsui,S. Novel serine protease BSSP6 Patent: WO 0031257-A 1 02-JUN-2000; FUSO PHARMACEUTICAL INDUSTRIES LTD, HIDEOTOSHI UEMURA, AKIRA OKUI, KATSUYA KOMINAMI, NOZOMI YAMAGUCHI, SHINICHI MITSUI			
COMMENT	OS Homo sapiens (human) PN WO 0031257-A/1			

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1258	100.0	1106	20	AAZ22638	CASB12 nucleotide
2	1258	100.0	1158	20	AAZ22639	CASB12 derived fro
3	1258	100.0	1186	24	ABK92131	Prostate cancer-as
4	1258	100.0	1186	25	ABX76468	Lung cancer-associ
5	1258	100.0	1186	22	AAD14842	Human PS133 gene c
6	1258	100.0	1204	21	AAA37072	Human P101279 (UNO
7	1258	100.0	1204	22	AAS21496	Human cDNA sequenc
8	1258	100.0	1204	22	AAFS4320	DNA encoding prote
9	1258	100.0	1204	24	ABL95664	Human angiotensin
10	1258	100.0	1204	24	ABL88175	Human P101279 cDNA
11	1258	100.0	1204	25	ABK33628	cDNA encoding huma
12	1258	100.0	1204	25	ACA03855	cDNA encoding huma
13	1258	100.0	1204	25	ACA04276	Human cDNA encodin
14	1258	100.0	1204	25	ABX98393	DNA encoding novel
15	1258	100.0	1292	22	ABA83372	Human secreted pro
16	1258	100.0	1301	21	AAA61763	cDNA encoding huma
17	1258	100.0	1314	21	AAZ30222	cDNA encoding a hu
18	1248	99.2	1146	20	AAV84589	Human secreted pro
19	1248	99.2	1146	22	ABA83430	Human secreted pro
20	1246	99.0	1166	22	AAD14841	Human PS133 consen
21	1235.5	98.2	934	21	AAA61765	cDNA encoding huma
22	1228	97.6	1191	20	AAZ97777	Extended human sec
23	1227.5	97.6	1335	21	AAZ45672	Nucleotide sequenc
24	1219.5	96.9	1052	21	AAZ87798	Activation constru
25	1219.5	96.9	1052	22	AAFS5270	Nucleotide sequenc
26	1213	96.4	833	19	AAV42925	DNA encoding a hum
27	1062	84.4	1323	21	AAA61764	cDNA encoding mous
28	1014.5	80.6	1164	24	ABBS1683	DNA encoding human
29	916.5	72.9	618	24	ABK30233	Human G-protein-co
30	829	65.9	762	21	AAH31050	Human colon cancer
31	829	65.9	762	21	AAH31061	Human colon cancer
32	736	58.5	1375	22	AAS26876	Human cDNA encodin
33	736	58.5	1438	24	ABQ99555	Human coding sequ
34	716	56.3	1365	22	AAS41087	cDNA encoding nove
35	716	56.9	924	22	AAS41622	cDNA encoding nove
36	716	56.9	924	22	AAS26948	Human cDNA encodin
37	716	56.9	924	23	ABK41855	cDNA encoding nove
38	684	54.4	1322	24	AB199534	Mouse ischaemic co
39	684	54.4	1333	17	AAT48519	Human neuropilin-en
40	684	54.4	1333	18	AAT63251	Mouse neuropilin ge
41	683	54.3	942	20	AAT11030	Human serine prote
42	682	54.2	963	24	AAD30570	Human proteinase, PR
43	682	54.2	963	24	ABK1774	DNA encoding novel
44	682	54.2	1278	24	ABK46347	cDNA encoding nove
45	681	54.1	809	23	AAS87560	DNA encoding novel

ALIGNMENTS

RESULT 1
AAZ22638
ID AAZ22638 standard; cDNA, 1106 BP.
AC AAZ22638;
XX
DT 08-DEC-1999 (first entry)
XX
DE CASB12 nucleotide sequence.
XX
KW neuropilin; cancer; assay; inhibitor; serine protease; immunogenic;
XX ds.
XX
OS Homo sapiens.
XX
FH Key
CDS Location/Qualifiers
14..862

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FT      /tag= a
XX      /product= CASB12
PN      WO9949055-A1.
XX      30-SEP-1999.
PD      17-MAR-1999; 99WO-EP01894.
XX      20-MAR-1998; 98GB-0006095.
XX      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA      Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;
XX      WPI; 1999-580450/49.
XX      P-PSDB; AAY42439.
XX      New human serine protease CASB12, for treatment, prevention and
PT      diagnosis of cancer and autoimmune diseases
XX
XX      Claim 10; Page 47; 58pp; English.
PS
XX      This is the nucleotide sequence of the CASB12 gene. The nucleotide
CC      sequence of AA222638 shows homology with neuropilin and the encoded
CC      protein AAY42439, is structurally related to other proteins of the
CC      serine protease family, having homology and/or structural similarity
CC      with neuropilin. It is expected that as well as similar structure, these
CC      proteins will also share similar biological functions and properties.
CC      The CASB12 polypeptides and polynucleotides can be used to develop
CC      methods for identifying agonists and antagonists/inhibitors of these
CC      molecules, and thereby treating conditions associated with CASB12
CC      polypeptide imbalance. The invention also provides for diagnostic assays
CC      for detecting diseases associated with inappropriate CASB12 polypeptide
CC      activity or levels.
CC      Since CASB12 is either specifically expressed or highly over-expressed
CC      in tumors compared to normal cells, the polypeptides and polynucleotides
CC      of the invention are believed to be important immunogens for specific
CC      prophylactic or therapeutic immunization against tumors. The
CC      polypeptides and polynucleotides can therefore be targeted by antigen
CC      specific immune reactions (which result in the destruction of the tumor
CC      cell) or they can be used to diagnose the occurrence of tumor cells.
XX
SQ      Sequence 1106 BP, 247 A; 348 C; 287 G; 224 T; 0 other;

Alignment Scores:
Pred. No.: 4.52e-105 Length: 1106
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x AA222638 (1-1106)
OY      1 I1e1e1e1ySG1yPhG1uCySLySProH1sSerG1nPOT1P1G1A1A1a1eupheG1u 20
DB      173 ATCATCAAGGGGTTGAGTGCAGCAAGCTCACTCCAGCCTTGACAGCAGCCCTGTTCCAG 232
OY      21 LysTThrArgLeuLeuCySG1yAlaThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB      233 AAGAGCGCGGCTACTGTGTGGGCGAGCGCTCATCGCCCGCAGATGGCTCTCTGACACAGCC 292
OY      41 HisCySLeUySPROArgTyrl1e1a1His1eUg1yG1nHis1aSn1eUg1n1ySG1uG1u 60
DB      293 CACTCCCTCAAGCCCGCTACTACTTCACTCGGGGCGAGCAACCTCCAGAAAGAGAGAG 352
OY      61 GlyCySG1uG1nThrArgThrAlaThrG1uSerPheProH1sProG1yPhe1aSn1sSer 80
DB      353 GGCTGTGAGAGACCCGAGACAGCCACTGAGTCTTCCCCACCCCGGCTTCAACAACAGC 412
OY      81 LeuProAn1yASpH1sArg1aSn1sP1eU1eU1eU1eU1eU1eU1eU1eU1eU1eU1eU 100

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DB      413 CTCGCCAACAAGACACCCGATGACATCATGCTGTGAAAGATGCATGCCAGTCTCC 472
OY      101 I1eThrTrpAlaValArgProLeuThrLeuSerSerArgCyVal1ThrAlaG1yThrSer 120
DB      473 ATCACTGGGCTGTGCGACCCCTCACCCTCTCTCAGCGCTGTGCATCGTGGCAGCAGC 532
OY      121 CysLeu1leSerG1yTP1G1ySerThrSerSerProG1nLeuAlaG1eUProH1sTh1eU 140
DB      533 TGCTCATTTTCGGCTGGGCGAGCAGCTCCAGCCCCAGTTACCGCTGCTCAACACCTTG 592
OY      141 ArgCySa1aSn1leThr1le1e1G1uH1sG1n1yCySG1uA1aSn1a1aTy1ProG1yA1a 160
DB      593 CGATGCCCAACATCACCATTATTGAGCACCAGAAAGTGTGAAGCGCTTACCCGGCAAC 652
OY      161 I1eThrAspThrMetValCySa1aSerValG1nG1uG1y1yAspSerCySG1nG1y 180
DB      653 ATCACAGACACATGATGTGTGTGCAGCGTGCAGGAAGGGGCGCAAGCACTCCTGCCAGGCT 712
OY      181 AspSerG1yG1yProLeuValCySa1nG1nSer1eUng1y1le1eSerTrpG1yG1n 200
DB      713 GACTCCGGGGCCCTCTGTGTGTGAACCACTCTCTCAAGGCATTATCTCTGGGGCCAG 772
OY      201 AspProCySa1a1eThrArgLySPROG1yValTyThrLyValCySLyTyValAsp 220
DB      773 GATCCGTGTGCGATCACCCGAAACCTGTGTCTTACAGAAAGTCTGCAAAATATGTGAC 832
OY      221 Trp1leG1nG1uThrMetLySa1aSn 229
DB      833 TGATCCGAGAGACGATGAAGAACAT 859

RESULT 2
AA222639
ID      AA222639 standard; cDNA; 1158 BP.
XX
AC      AA222639;
XX
DT      08-DEC-1999 (first entry)
XX
DE      CASB12 derived from Expressed Sequence Tag sequences.
XX
KW      neuropilin; cancer; assay; inhibitor; serine protease; immunogenic;
XX      autoimmune disease; ds.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      CDS 84..932
FT      /tag= a
FT      /product= CASB12
XX
PN      WO9949055-A1.
PD      30-SEP-1999.
XX
XX      17-MAR-1999; 99WO-EP01894.
DR      WPI; 1999-580450/49.
XX      P-PSDB; AAY42440.
XX      New human serine protease CASB12, for treatment, prevention and
PT      diagnosis of cancer and autoimmune diseases
XX
XX      Claim 26; Page 49; 58pp; English.
XX
XX      This is the nucleotide sequence of the CASB12 gene derived from
CC      Expressed Sequence Tag (EST) search for tumor-specific and
CC      tumor-associated antigens. The nucleotide sequence of AA222638 shows

```

CC homology with neuropsin and the encoded protein AAV42439 is structurally
CC related to other proteins of the serine protease family, having homology
CC and/or structural similarity with neuropsin. It is expected that as well
CC as similar structure, these proteins will also share similar biological
CC functions and properties.
CC The CASB12 polypeptides and polynucleotides can be used to develop
CC methods for identifying agonists and antagonists/inhibitors of these
CC molecules, and thereby treating conditions associated with CASB12
CC polypeptide imbalance. The invention also provides for diagnostic assays
CC for detecting diseases associated with inappropriate CASB12 polypeptide
CC activity or levels.
CC Since CASB12 is either specifically expressed or highly over-expressed
CC in tumors compared to normal cells, the polypeptides and polynucleotides
CC of the invention are believed to be important immunogens for specific
CC prophylactic or therapeutic immunization against tumors. The
CC polypeptides and polynucleotides can therefore be targeted by antigen
CC cell immune reactions (which result in the destruction of the tumor
CC cell) or they can be used to diagnose the occurrence of tumor cells
XX
XX Sequence 1158 BP; 274 A; 359 C; 306 G; 219 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 4,8e-105 Length: 1158
XX Score: 1258.00 Matches: 229
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: Gaps: 0
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US-09-856-320A-2_COPY_54_282 (1-229) x AAZ22639 (1-1158)
QY 1 llellellygslpheglucyslyspromhissergslprrtrnglnalaaleuphegu 20
DB 243 ATCATAAAGGGGTTCCAGTGCAGCAAGCTCACTCCACCCCTGGAGGACGCTGTTCGAG 302
QY 21 lvsythargleuencysgslalathrleuilealproargtrpreuethrallaala 40
DB 303 AAGACCGGGCTACTGTGGGGGAGCGCTCATGCCCCCAGATGGCTCTCGACAGACGC 362
QY 41 Hiscysleuylspproargtrylevalhlsleuglyghlhisasleuenglnylsglgu 60
DB 363 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGACACAACTCCAGAAAGAGAG 422
QY 61 Glycysgluglthrrhrrhrrhrrhrrhrrhrrhrrhrrhrrhrrhrrhrrhrrhrrhrr 80
DB 423 GGGTGGAGAGAGCCGAGACGCTGAGTCTCTCCACCCCGCTTCAACACACAGC 482
QY 81 Leuproasnlylsasphlsaraganaepillemetleuvallysmecalaaserprovalser 100
DB 483 CTCGCCAACAAGACACCGCAATGACATCATCTGTGTAAGATGCGCATCGCATCTGC 542
QY 101 llethrrpalaavalarproleuthrrleuserserargcysvalthrilaaglythrser 120
DB 543 ATACACCTGGGCTGTGTGACCCCTCACTCTCTCTCAAGCTGTGTCCTGTGGACACAGC 602
QY 121 Cysleuilelsergsllytrpglyserthrserserproglhnuargleuprohisrthrleu 140
DB 603 TCCCTCATTTCCGGCTGGGGGAGACAGTCAAGCCCCCACTTACGCTGTCTACACACTTG 662
QY 141 Argcysalaasnillethrrillellegluhlsiglnlycysgluasnulatyrprogliaasn 160
DB 663 CGATGGCCCAACATCACTCATTTGACACACAGAGTGTGAAGACCCCTACCCCGGCAAC 722
QY 161 llethrraspthrmevalcysalaservalglingllyllylsaspserserCysglingly 180
DB 723 ATCACAGACACCATGGTGTGTGTCCAGCGTGCAGAAAGGGGAGACACTCTGCCAGGCT 782
QY 181 Aspsergslglyproleuvalcysaanglnserleuenglnlyllellesertrpglygin 200
DB 783 GACTCCGGGGGGCCCTGTGTGTGTACCAAGTCTCTTCAAGGCAATATCTCCGGGGCCAG 842
QY 201 AspProCysAlaIleThrrglusProgllyValTyrThlyValCyslystYrValAasp 220

DB 843 GATCCGTGTGCATCACCCGAAAGCTGTGTCTACACGAAGTGTCAATATGTGAC 902
QY 221 Trrpilleglugluthrmetlysasnsen 229
DB 903 TGGATCCAGAGACGATGAAGAAACAT 929
RESULT 3
ID ABR92131 standard; DNA; 1186 BP.
XX ABR92131;
XX AC ABR92131;
XX AC ABR92131;
XX 15-AUG-2002 (first entry)
XX DT
XX DE Prostate cancer-associated DNA sequence #17.
XX DE
XX KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
XX KW gene therapy; gene; ds.
XX OS Mammalia.
XX PN WO200230268-A2.
XX PD 18-APR-2002.
XX XX
XX 12-OCT-2001; 2001WO-US32045.
XX PF
XX 13-OCT-2000; 2000US-0687576.
XX PR 08-DEC-2000; 2000US-0733288.
XX PR 08-DEC-2000; 2000US-0733742.
XX PR 24-JAN-2001; 2001US-263957P.
XX PR 16-MAR-2001; 2001US-276791P.
XX PR 16-MAR-2001; 2001US-276888P.
XX PR 06-APR-2001; 2001US-281922P.
XX PR 24-APR-2001; 2001US-286214P.
XX PR 30-APR-2001; 2001US-0847046.
XX PR 04-MAY-2001; 2001US-288589P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX XX
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevez P;
PI
XX P-PSDB; ABR61816.
XX DR MPI: 2002-471335/50.
XX XX
XX PT Detecting a prostate cancer-associated transcript in a cell in a
XX PT patient, useful for diagnosing prostate cancer (PC) or screening
XX PT modulators of PC, by determining if prostate cancer-associated genes
XX PT are expressed in a prostate tissue
XX
XX Claim 22; Page 313; 436pp; English.
XX PS
XX XX
XX The present invention relates to methods of detecting a prostate
XX cancer-associated transcript in a cell from a patient. The method
XX comprises contacting a biological sample from the patient with
XX prostate cancer-associated polynucleotides (designated PC genes) that
XX selectively hybridize to a sequence that is at least 80% identical
XX to them. The prostate cancer-associated polynucleotide sequences
XX are differentially expressed in prostate tumour tissue or in
XX prostate cancer and are derived from the tissues of various
XX organisms such as humans or other mammals (e.g. mice, sheep and dogs).
XX The methods of the invention are useful for diagnosing and treating
XX prostate cancer in mammals. The prostate cancer-associated genes are
XX useful for diagnosing or treating prostate cancer, as well as for
XX identifying modulators of prostate cancer or agents that inhibit
XX prostate cancer. The nucleic acid sequences are particularly useful
XX in gene therapy, as a vaccine or in antisense applications.
XX ABR92115-ABR92263 represent prostate cancer-associated polynucleotide
XX sequences.
XX
XX Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other;
XX
XX Alignment Scores:

Pred. No.: 4,95e-105 Length: 1186
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-856-320a-2_copy_54_282 (1-229) x ABX92131 (1-1186)

QY 1 llellelysglypnehlucylsyserprohisergerinprotrpglnalalauphegu 20
 DB 185 ATCATCAAGGGGTTGAGTGCAGAGCTCAGTCCAGCCCTGGCAGGAGCCCTGTTCCAG 244
 QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrPLeuLeuThraAla 40
 DB 245 AAGACGGGCTACTGTGGGGGCGAGGCTCATCGCCCGAGATGGCTCTGACAGCAGCC 304
 QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlu 60
 DB 305 CACTGCCTCAAGCCCGCTACATAGTTCACTGGGGGCGAGCACAACCTCCAGAGAGAG 364
 QY 61 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80
 DB 365 GCGTGTGAGCAGACCCGAGCAGCAGCTAGTCTTCCCCAGCCCGGCTTCAACAAGC 424
 QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
 DB 425 CTCCCAACCAAGACACCGCAATCATGATGCTGGTGAATGATGCAATCGCAGTCTCC 484
 QY 101 lleThrTPAlaValArgProheuthrleuserSerArgCysValThrAlaGlyThrSer 120
 DB 485 ATCAGCTGGGCTGTGGACCCCTCACTCTCTCAAGTGTCACTGCTGGCAGCAGC 544
 QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
 DB 545 TGCCCATTTCCGGGCGGGGCGAGCAGTCAACCCCGAGTTAGGCTGCTCAGACCTTG 604
 QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
 DB 605 CGATCGGCGCAATCATCATCTTGAAGCAGCAGAAAGTGAAGACGCCCTACCCCGGCAAC 664
 QY 161 lleThrArgProMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180
 DB 724 665 ATCAGAGACCATGATGTGTCCAGCGGAGAGGGGGGAGAGACTCTCCAGAGGT 724
 QY 181 AspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrPLeuGln 200
 DB 784 725 GACTCCGGGGGCGCTCTGTGTGAACAGTCTCTTCAAGGATTAATCTCCGGGGCCAG 784
 QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
 DB 844 785 GATCCGTGTGCATCAACCGAAAGCTGTGTCTACAGAAAGTCTGCAATATATGTGAC 844
 QY 221 TrrPLeuGlnGluThrMetLysAsnAsn 229
 DB 845 TGGATCCAGAGACGATGAAGAACAT 871
 RESULT 4
 ABX76468
 ID ABX76468 standard; DNA; 1186 BP.
 AC ABX76468;
 DT 02-APR-2003 (first entry)
 XX Lung cancer-associated polynucleotide #312.
 DE Lung cancer-associated polynucleotide #312.
 XX Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

OS Unidentified.
 XX WO200286443-A2.
 PN 31-OCT-2002.
 XX 18-APR-2002; 2002WO-US12476.
 PF 18-APR-2002; 2002US-284770P.
 XX 18-APR-2001; 2001US-284770P.
 PR 10-MAY-2001; 2001US-290492P.
 PR 09-NOV-2001; 2001US-339245P.
 PR 13-NOV-2001; 2001US-350666P.
 PR 29-NOV-2001; 2001US-334370P.
 PR 12-APR-2002; 2002US-372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 PA
 PI Aziz N. Murray R;
 XX WPI: 2003-093161/08.
 DR P-PSDB; ABU56739.
 XX

PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer -
 PS
 XX Claim 22; Page 443; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung
 CC cancer-associated polynucleotides and polypeptides are used for
 CC identifying a compound that modulates a lung cancer-associated
 CC polypeptide, for inhibiting proliferation of a lung cancer-associated
 CC cell to treat lung cancer in a patient and for treating a mammal having
 CC lung cancer by administering a modulatory compound identified. The
 CC methods are useful for treating lung cancer, such as small cell lung
 CC cancer, non-small cell lung cancer or other benign or precancerous
 CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
 CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
 CC and polypeptides are useful for diagnostic purposes and as targets for
 CC screening for therapeutic compounds that modulate lung cancer, such as
 CC antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated
 CC polynucleotides of the invention.

XX Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other:

Alignment Scores:

Pred. No.: 4,95e-105 Length: 1186
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0

US-09-856-320a-2_copy_54_282 (1-229) x ABX76468 (1-1186)

QY 1 llellelysglypnehlucylsyserprohisergerinprotrpglnalalauphegu 20
 DB 185 ATCATCAAGGGGTTGAGTGCAGAGCTCAGTCCAGCCCTGGCAGGAGCCCTGTTCCAG 244
 QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrPLeuLeuThraAla 40
 DB 245 AAGACGGGCTACTGTGGGGGCGAGGCTCATCGCCCGAGATGGCTCTGACAGCAGCC 304
 QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlu 60
 DB 365 CACTGCCTCAAGCCCGCTACATAGTTCACTGGGGGCGAGCACAACCTCCAGAGAGAG 364

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QY 61 GlyCysGluGlnThrArgThrAlaThrGlnGluSerPheProHisProGlyPheAsnAsnSer 80
DB 365 GGCTGTGAGACAGACCCGGACAGCAGCTGAGTCTTCCCCACCCGGCTTCAACAAACAG 424
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 425 CTCCCAACAAACACACCGCAATGACATCATCTGCTGTAAGATGAGCATGCGCAGTCTCC 484
QY 101 IleThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 485 ATCACTGGGCTGTGGACCCCTCACCCTCTCTCAAGCTGTGTCACTGTGGCACCAG 544
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 545 TGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCACTGACCTGCTGCACACTTG 604
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
DB 605 CGATGCGCCACATCATCATATGAGCACACAGAAAGTGTAGAACCCCTAACCCGGCAAC 664
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
DB 665 ATCAGACACCATGATGTGTGTCCAGCTGCAGAAAGGGGCAAGGACTCTGCGAGGT 724
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB 725 GACTCGGGGGCCCTGTGTGTGTACAGCTCTTCAAGGCAATATCTCTGGGGCCAG 784
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
DB 785 GATCCGCTGTGCATCACCCGAAAGCTGTGTCTACAGAAAGTGCAGAAATATGTGAC 844
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
DB 845 TGGATCAGAGACGATGTGTGTCCAGCTGCAGAAAGGGGCAAGGACTCTGCGAGGT 871

RESULT 5
AADI4842
ID AADI4842 standard; DNA; 1192 BP.
XX AADI4842;
AC AADI4842;
XX
XX 01-NOV-2001 (first entry)
XX
XX Human PS133 gene contig.
XX
XX Human; PS133; prostate disease; cancer; immunogen; gene therapy; EST;
XX expressed sequence tag; cytostatic; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 107..859
XX /*tag= a
XX /product= "Human PS133 protein"
XX /transl_except= (pos:188..196, aa:Cys-Pro)
XX /transl_except= (pos:224..232, aa:Phe-Lys)
XX
XX US6232456-B1.
XX
XX 15-MAY-2001.
XX
XX 06-OCT-1997; 97US-0944483.
XX
XX 06-OCT-1997; 97US-0944483.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Cohen M, Colclitts TL, Friedman PN, Granados E, Klass MR;
XX Russell JC, Stewart KD, Stroupe SD;
XX WPI; 2001-366357/38.
XX
XX P-PSDB; AAE08017.

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XX
XX New PS133 polynucleotides, useful for detecting, diagnosing, staging,
XX PT monitoring, prognosing, preventing, treating or determining the
XX PT predisposition of an individual to a prostate disease, e.g. cancer -
XX Claim 1, Column 71-74; 93pp; English.
XX
XX The patent discloses PS133 polynucleotides and polypeptides which
XX are indicative of prostate disease. The patent also provides a method
XX for detecting PS133 protein in a test sample. The polynucleotides of
XX the invention are useful for detecting, diagnosing, staging, monitoring,
XX prognosing, preventing, treating or determining the predisposition of
XX an individual to prostate diseases such as cancer. PS133-derived
XX polynucleotides are used for the detection of normal or altered gene
XX expression, in assays for detecting, amplifying or quantifying genes
XX or nucleic acids relating to prostate tissue diseases and conditions,
XX and to produce probes which can be used in the detection of nucleic
XX acids in a sample. PS133 proteins are used as immunogens for the
XX production of antibodies. PS133 sequences are also used in gene
XX therapy. The present sequence is human PS133 gene contig.
XX
XX Sequence 1192 BP; 279 A; 385 C; 290 G; 238 T; 0 other;
XX
XX

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Alignment Scores:

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Pred. No.: 4,98e-105 Length: 1192
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

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US-09-856-320A-2_COPY_54_282 (1-229) x AADI4842 (1-1192)

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QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTyrGlnAlaLeuPheGln 20
DB 170 ATCATCAAGGGGTTGAGTGCAGCAAGCTCCTCCAGCCCTGGCAGGACCCCTGTCGAG 229
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40
DB 230 AAGAGCGGCTACTGTGTGGGGGAGCGCTCATCGCCCAAGATGCTCTGTGACAGAGCC 289
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlnGlnHisAsnLeuGlnGlnGlu 60
DB 290 CACTGCTCTAAGCCCCCGCTACATAGTTCACTCGGGGACAGACAACTCCAGAGAGAG 349
QY 61 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80
DB 350 GGCTGTGAGACAGACCCGGACAGCAGCTGAGTCTTCCCCACCCGGCTTCAACAAACAG 409
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 410 CTCCCAACAAACACACCGCAATGACATCATGCTGTGTAAGATGAGCATGCGCAGTCTCC 469
QY 101 IleThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 470 ATCACTGGGCTGTGGACCCCTCACCCTCTCTCAAGCTGTGTCACTGTGGCACCAGC 529
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 530 TGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCACTGACCTGCTGCACACTTG 589
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
DB 590 CGATGCGCCACATCATCATATGAGCACACAGAAAGTGTAGAAAGCCCTAACCCGGCAAC 649
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
DB 650 ATCAGACACCATGATGTGTGTCCAGCTGCAGAAAGGGGCAAGGACTCTCTGCAAGGT 709
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB 710 GACTCGGGGGCCCTGTGTGTGTACAGCTCTTCAAGGCAATATCTCTGCGGGGCCAG 769

```

QY 201 AspProCysAlaIleThrArgIysProGlyValTyrThrIysValCysIysTyrValAsp 220
 DB 770 GATCGGTGCGCATCACCGAAAGCCTGCTGTCTACACGAAAGTGTGCAAAATATGTGAC 829
 QY 221 TrpIleGlnGluThrMetIysAsnAsn 229
 DB 830 TCGATCCAGACACGATGAGAACAAAT 856
 RESULT 6
 AAA37072
 ID AAA37072 strand; cDNA, 1204 BP.
 AC AAA37072;
 XX 08-AUG-2000 (first entry)
 DT Human PRO1279 (UNQ649) cDNA sequence SEQ ID NO:169.
 XX
 DE Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
 KM transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
 KW ss.
 OS Homo sapiens.
 XX MO200012708-A2.
 PN 09-MAR-2000.
 XX
 PD 01-SEP-1999; 99WO-US20111.
 XX
 PF 01-SEP-1998; 98US-0098716.
 PR 01-SEP-1998; 98US-0098749.
 PR 01-SEP-1998; 98US-0098750.
 PR 02-SEP-1998; 98US-0098803.
 PR 02-SEP-1998; 98US-0098821.
 PR 02-SEP-1998; 98US-0098843.
 PR 09-SEP-1998; 98US-0099536.
 PR 09-SEP-1998; 98US-0099596.
 PR 09-SEP-1998; 98US-0099598.
 PR 09-SEP-1998; 98US-0099602.
 PR 09-SEP-1998; 98US-0099642.
 PR 10-SEP-1998; 98US-0099741.
 PR 10-SEP-1998; 98US-0099754.
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 PR 10-SEP-1998; 98US-0099792.
 PR 10-SEP-1998; 98US-0099808.
 PR 10-SEP-1998; 98US-0099812.
 PR 10-SEP-1998; 98US-0099815.
 PR 10-SEP-1998; 98US-0099816.
 PR 15-SEP-1998; 98US-0100385.
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 PR 15-SEP-1998; 98US-0100390.
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 PR 16-SEP-1998; 98US-0100662.
 PR 16-SEP-1998; 98US-0100664.
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 PR 18-SEP-1998; 98US-0101068.
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 PR 23-SEP-1998; 98US-0101475.

PR 23-SEP-1998; 98US-0101476.
 PR 23-SEP-1998; 98US-0101477.
 PR 23-SEP-1998; 98US-0101479.
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 PR 24-SEP-1998; 98US-0101741.
 PR 24-SEP-1998; 98US-0101743.
 PR 24-SEP-1998; 98US-0101915.
 PR 24-SEP-1998; 98US-0101916.
 PR 29-SEP-1998; 98US-0102207.
 PR 29-SEP-1998; 98US-0102240.
 PR 29-SEP-1998; 98US-0102307.
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 PR 29-SEP-1998; 98US-0102331.
 PR 30-SEP-1998; 98US-0102484.
 PR 30-SEP-1998; 98US-0102487.
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 PR 01-OCT-1998; 98US-0102684.
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 PR 02-OCT-1998; 98US-0102965.
 PR 06-OCT-1998; 98US-0103258.
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 PR 08-OCT-1998; 98US-0103633.
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 PR 08-OCT-1998; 98US-0103679.
 PR 08-OCT-1998; 98US-0103711.
 PR 14-OCT-1998; 98US-0104257.
 PR 20-OCT-1998; 98US-0104987.
 PR 20-OCT-1998; 98US-0105000.
 PR 20-OCT-1998; 98US-0105002.
 PR 21-OCT-1998; 98US-0105104.
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 PR 22-OCT-1998; 98US-0105266.
 PR 26-OCT-1998; 98US-0105693.
 PR 26-OCT-1998; 98US-0105694.
 PR 27-OCT-1998; 98US-0105807.
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 PR 29-OCT-1998; 98US-0106248.
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 PR 30-OCT-1998; 98US-0106454.
 PR 03-NOV-1998; 98US-0106856.
 PR 03-NOV-1998; 98US-0106902.
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 PR 03-NOV-1998; 98US-0106919.
 PR 03-NOV-1998; 98US-0106932.
 PR 03-NOV-1998; 98US-0106934.
 PR 10-NOV-1998; 98US-0107783.
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 PR 17-NOV-1998; 98US-0108802.
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 PR 17-NOV-1998; 98US-0108807.
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 PR 17-NOV-1998; 98US-0108925.
 PR 18-NOV-1998; 98US-0108848.

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PR 18-NOV-1998; 9805-0108849.
PR 18-NOV-1998; 9805-0108850.
PR 18-NOV-1998; 9805-0108851.
PR 18-NOV-1998; 9805-0108852.
PR 18-NOV-1998; 9805-0108858.
PR 18-NOV-1998; 9805-0108904.
XX
XX (GETH ) GENENTECH INC.
XX
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
DR WPI, 2000-237871/20.
DR P-PSDB; AAY93390.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/ligand interactions
XX
XX Claim 2; Fig 101; 773pp; English.
XX
XX - AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY9340 to AAY9462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
CC PCR primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention.
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XX SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:
Pred. No.: 5.04e-105 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

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QY 1 IleIleIleGlyGlyPheGluCysLysProHisSerGlnProTroglnAlaIleuPheGlu 20
DB 169 ATCATCAAGGGGCTTCAGAGTCAAGCTTCACTCCCAAGCTGGGAGGAGGCTTTCGAG 228
QY 21 LysThrArgLeuLeuLeuGlyAlaThrLeuIleAlaProArgTyrPheLeuThrAlaAla 40
DB 229 AAGACCGGCGTACTCTGTGGGGGAGCGCTCATGCGCCCAAGATGGCTCTGACAGCAGCC 288
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
DB 289 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGACACCAATCCAGAGGAGGAG 348
QY 61 GlyCysGluGlnThrArgThrAlaThrGlnLysPheProHisSerProGlyPheAsnAsnSer 80
DB 349 GGCTGTGACAGACAGCCGAGCAGCTGAGTCTTCCCAAGCTGGGCTTCAACAGCAGC 408
QY 81 LeuProAsnLysAspHisArgAsnAspGlnMetLeuValLysMetAlaSerProValSer 100
DB 409 CTCGCCCAAGCAAGACAGCAGCATGATGATGCTGTAAGATGAGCATGCGCAGCTCC 468
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 469 ATCACTGGGGCTGTGGAGCCCTCAACCTCTCTCAAGCTGTGATCACTGGCAGCAGC 528
QY 121 CysLeuLysSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 529 TGCCTCATTTCCGGCTGGGGGAGCAGCTCAAGCCCAATTACGCTGCTACACCTTG 588
QY 141 ArgCysAlaAsnLysThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
DB 589 CGATGGCCCAACATCACTCATTTGAGCAGCAGAAAGTGTGAGAGAGCCCTACCCGGCAAC 648

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QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 180
DB 649 ATCAAGACACCATGGTGTGTGTGACAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGG 708
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGln 200
DB 709 GACTCCGGGGGGCCCTTGTGTGTGTACAGAGTCTTCAAGGCAATTATCTCTGGGGCCAG 768
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
DB 769 GATCCGTTGTCATCAACCCGAAAGCCTGGTGTCTACACGAAGTGTCAAAATGTGTGAC 828
QY 221 TrpIleGlnLysThrMetLysAsn 229
DB 829 TGTATCCAGAGACGATGAAGAAAT 855

RESULT 7
AAS21496
ID AAS21496 strand; cDNA; 1204 BP.
XX
XX AAS21496;
AC
XX
XX 24-OCT-2001 (first entry)
DT
XX
DE Human cDNA sequence encoding for PRO1279 polypeptide.
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
XX adipocyte; A-peptide; factor VIIA; gene therapy; se.
XX
OS Homo sapiens.
XX
XX WO200140466-A2.
PN
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
XX 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;

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XX WPI: 2001-408281/43.
 DR P-PSDB; AAU12424.
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 PS Claim 3; Fig 505; 813bp; English.
 XX
 CC AAS1244-AAS21518 encode for novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 5 04e-105 Length: 1204
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
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 DB 169 ATCATCAAGGGGTTGAGTGAAGAGCTCCTCCAGCCCTGGCAGGACCCCTGTTGAG 228
 QY 21 lvsfthrtglsleuueucysgllyalathrleullealeaaproarytrpleuleuthralaala 40
 DB 229 AAGAGCGGGCTACTCTGTGGGGCGAGCGCTCATCGCCCAAGATGGCTCTGCACACAGC 288
 QY 41 Hiscysleuylspproarytrylevalhslauglyglnhisasnleuglnlysglgu 60
 DB 289 CACTGCTTAAGCCCGCCGCTACATAGTTCACTGGGGCAGACAACTCCAGAGAAGGAG 348
 QY 61 glycysgluglnthrtgthralathrgluserpheprohisproglypheasnaanser 80
 DB 349 GGCTGTGACAGACCCGAGCAGCACTAGTCTTCCACCCCGGGCTTCAACAACAGC 408
 QY 81 leuproasnlyasphisaargasnbspllethleuvallymetalasereprovalser 100
 DB 409 CTCCCCAACMAAGACACCGCAGCATATGATGCTGTGAMATGATGCATCGCCAGCTCC 468
 QY 101 llettrtpalaivalarproleuthrleuserserargcysvalthralaglythrser 120
 DB 469 ATCACTGGGCTGTGGACCCCTCACTCTCTCTCAAGTGTGATCTGTGGACCCAGC 528
 QY 121 Cysleuileserglytrpqlyserthrserseproglinleuarleuprohisthrleu 140
 DB 529 TGCCATATTTCCGGGCGGAGCAGGTCCACCCCAAGTTAGCGCTGCTCACACCTTG 588
 QY 141 Argcysalaasnllethrilleleghisglnlycysgluasnalaatyproglyasn 160

DB 589 CGATGCGGCAACATCATCATTTGAGCAGCAGAGTGTGAAAGCCTTACCCCGGCAC 648
 QY 161 lletthraepthrmeevalcysalaservalglnuglylylsaspserecysglnly 180
 DB 649 ATCAACAGACACATGCTGTGTGCGCAGCTGCAGAGAGGGGCAAGACTCTTCCAGGCT 708
 QY 181 aspseryglylyproleuvalcysasnlnserleuglnlylleisertrpqlgln 200
 DB 709 GACTCCGGGGCCCTCTGTGCTGTATACCAAGCTCTTCAAGGCATATCTCTCGGGGCCAG 768
 QY 201 aspprocsalalietthrtarglyseproglyvaltythrlyrsvalcyslvetryvalasp 220
 DB 769 GATCGGTGTGATCATCCCGAAGCCTGTGTCTTACAGAAAGTCTGCAATATGTGAC 828
 QY 221 trpilleglnlurtmrmetlyasnaasn 229
 DB 829 TGGATCCAGACGACGATCAAGACAT 855
 RESULT 8
 AAF54320
 ID AAF54320 standard; DNA; 1204 BP.
 XX
 AC AAF54320;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE DNA encoding protein of the invention #51.
 XX
 KW Secreted; transmembrane; gene therapy; ss.
 XX
 OS Unidentified.
 XX
 PN WO200078961-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04342.
 XX
 PR 23-JUN-1999; 99US-0141037.
 XX
 PR 20-JUL-1999; 99US-0144758.
 XX
 PR 26-JUL-1999; 99US-0145698.
 XX
 PR 01-SEP-1999; 99WO-US20111.
 XX
 PR 29-OCT-1999; 99US-0162506.
 XX
 PR 30-NOV-1999; 99WO-US28313.
 XX
 PR 02-DEC-1999; 99WO-US28551.
 XX
 PR 16-DEC-1999; 99WO-US30095.
 XX
 PR 05-JAN-2000; 2000WO-US00219.
 XX
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Baton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Pan J, Peoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
 PI Watanabe CK, Williams PM, Wood WI;
 DR WPI: 2001-071395/08.
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy -
 PS Claim 2; Fig 101; 787bp; English.
 XX
 CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of
 CC anti-sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents.
 CC The nucleic acids may also be used in gene therapy.
 XX

Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5.04e-105	1258.00	100.00%	100.00%	100.00%	1204	229	0	0	0	0

US-09-856-320a-2_COPY_54_282 (1-229) x AAF54320 (1-1204)

```

QY      1  llellelygslpneglucyslyspromhserserglprotrpinaiaaleupheglu 20
DB      169  ATCATCAAGGGGTTCCAGTCCAGCTCTCCACGCCCGGAGGACGCCCTGTTCCAG 228
QY      21  lvsfthargleuleucysglvalatthrleuilealiproargtrpleuleuthralaia 40
DB      229  AAGACCCGGCTACTGCTGGGGCGAGCGCTATCGCCCCCAGATGCTCTCGACAGCAGCC 288
QY      41  HsCysleuileuproargtrprrilevalhileuGlyGlnHsasnleuGlnysglu 60
DB      289  CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGACACAACTCCAGAAAGGAGGAG 348
QY      61  GlyCysgluglnthrzargthralatthrGlyserPheProHiasProGlyPheasnaenser 80
DB      349  GGGTGGACAGACGCCGGACGACGACTGAGTCTTCCCGCCCGGCTTCAACAAACAGC 408
QY      81  leuproasnlysaaphisargasnaapliemelleuvallysmelaaserprovalser 100
DB      409  CTCGCCAACAAGACACCGCAATGACATCATCTGTAAGATGCGATCGCCAGTCTCC 468
QY      101  llethtralaivalrproleuthrleuserserArgCysValthrIaglythrser 120
DB      469  ATCACTGGAGCTGTGGACCCCTCACCTCTCTCAAGCTGTGTCACTGTGGACACAGC 528
QY      121  CysleuileserGlytrpGlyserThrSerSerProGlnleuargleuprohisThrleu 140
DB      529  TGGCTATTTCCGGCTGGGGGACGACGCTCCAGGCCCACTTACGCTTACACCTTGG 588
QY      141  ArgCysalaasnlethrIleileglnhsglnlyscysgluasnaIatYrProGlyAaen 160
DB      589  CGATGGCCAAACATCACTCATTCATGAGCACCAAGATGAGAACCCCTACCCGGCAAC 648
QY      161  llethAspThrmetvalcysalaserValGlnGlnGlylyAspserCysglnGly 180
DB      649  ATCAACAGACACCATGGTGTGTGCGACGTCGAGGAAGGGGCGAGGACATCTGCGAGGT 708
QY      181  AspserGlyGlyProleuValcysaenglnserleuGlnGlyIleiserTrpGlyGln 200
DB      709  GACTCGGGGGGCCCTCTGGTCTGTATACAGCTCTTCAAGGCAATTATCTCTGGGGCCAG 768
QY      201  AspProCysalaIlethrarglysproglyvalYrThrlyleValCyslystYrValaap 220
DB      769  GATCCGCTGGCGATCAACCGAAAGCTGTGTCTACACAAAGTGTGCAATATATGTGAC 828
QY      221  TrpIleGlnGlyThrmetlysasnaen 229
DB      829  TGGATTCAGAGACGATGAAGAACAT 855

```

RESULT 9

ABL95664
ID ABL95664 standard; cDNA; 1204 BP.
XX ABL95664;
XX
XX 19-JUL-2002 (first entry)
DE Human angiogenesis related cDNA PRO1279 SEQ ID NO: 207.
XX
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cyostatic; antiangiogenic; hypotensive; vulnerary;

```

KW      antiarteriosclerotic; gene; ss.
XX
XX Homo sapiens.
XX WO200208284-A2.
XX
XX 31-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-US21735.
XX
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222595P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 07-SEP-2000; 2000US-230978P.
XX 15-SEP-2000; 2000US-000000P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242922P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-MAR-2001; 2001WO-US06666.
XX 09-MAR-2001; 2001US-0802706.
XX 14-MAR-2001; 2001US-0808689.
XX 22-MAR-2001; 2001US-0816744.
XX 05-APR-2001; 2001US-0828366.
XX 10-MAY-2001; 2001US-0854208.
XX 10-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001US-0866028.
XX 25-MAY-2001; 2001US-0866034.
XX 25-MAY-2001; 2001WO-US17092.
XX 30-MAY-2001; 2001US-0870574.
XX 30-MAY-2001; 2001WO-US17443.
XX 01-JUN-2001; 2001WO-US17800.
XX 20-JUN-2001; 2001WO-US19692.
XX 28-JUN-2001; 2001WO-US00000.
XX
XX (GETH ) GENENTECH INC.
XX (BAKE/) BAKER K P.
XX (FERR/) FERRARA N.
XX (GERB/) GERBER H.
XX (GERR/) GERRITSEN M E.
XX (GODD/) GODDARD A.
XX (GODO/) GODOWSKI P J.
XX (GURN/) GURNEY A L.
XX (HILL/) HILLAN K J.
XX (HILL/) HILLAN K J.
XX (MARS/) MASTERS S A.
XX (MARS/) MASTERS S A.
XX (PANJ/) PAN J.
XX (PAON/) PAONI N F.
XX (STEP/) STEPHAN J F.
XX (MATR/) MATANABE C K.
XX (WILL/) WILLIAMS P W.
XX (WOOD/) WOOD W I.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
XX Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF,
XX Stephan JF, Matanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-171999/22.
XX P-PsDB; ABB95526.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

```

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 1, Fig 207; 567bp; English.

XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention.

XX SQ Sequence 1204 BP; 306 A; 364 C; 234 G; 240 T; 0 other;

Alignment Scores:

Pred. No.: 5 04e-105 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-856-320a-2_copy_54_282 (1-229) x ABL95664 (1-1204)

QY 1 ILEILEYSGLYPHGGLCYSLYSPROHISSEGINPROITRPGINLAIALEUPHEGII 20
DB 169 ATCATCAAGGGGTGAGTGAAGAGCTCACTCCAGCCCTGGCAGGACACCTGTTGAG 228
QY 21 LYSTHARGLEULEUCYSGIYALATHLEULEIALEAPRATRTIPLEULETHRALAIA 40
DB 229 AAGAGCGCGGCTACTGTGGGGGAGCGCATCGCCCAAGATGGCTCTGTCACACAGCG 288
QY 41 HSCYSLYSPROHARGTGTILEVALHISLEUGLYGNIHISASLEUNGILNYSGLUGIU 60
DB 289 CACTGCTCAAGCCCGCTACATAGTTCACTCGGGGACACCACTCCAGAAAGAGGAG 348
QY 61 GLYCYGSLUGLINTHARGTHRALATHRGISERPHROHISPROGILYPHESANSSEAR 80
DB 349 GGCTGTGACAGACCGCGACAGCACTAGTCTTCCGCCACCGCGCTTCAACAACAGC 408
QY 81 LEUPROASLTYASPHISARGHANSAPLIELEULEVALYMEALASERPROVALSER 100
DB 409 CTCCTCCAAAGAACACCGCAATGATCATGCTGTGTAAATGAGCATCGCCAGTCTCC 468
QY 101 ILETHRTPLAIVALARGPROLEUTHLEUSERSERARGCYSAVALTHRALAGLYTHRSER 120
DB 469 ATCACTGGGGCTGTGGGACCTCTCCTCCTCAGCTGTGTCACTGCTGGACACGAC 528
QY 121 CYSLEUILESESGLYTRPGIYSETHRSERSEARPROGILNLEUARGLEUPROHISTHLEU 140
DB 529 TCCCTCATTTCCGGCTGGGGGACAGCTCCACCCCAAGTTACGCTGCTCACACCTTG 588
QY 141 ARGCYSAIAASNLIEHTHLEILEGNIHISGLNLYSCYSLAASNALATYRPROGLYASN 160
DB 589 CATATGGCCAAACATACATCATATGAGCACCAAGATGTGAACAAGCCATCCCGCAAC 648
QY 161 ILETHRASPETHMETVALCYSAIASERVALGINGLUGLYLYEASPSERCYSGINGLY 180
DB 649 ATCAGACGACCATGTGTGTCCAGCGTGCAGGAAGGGGGAGAGACTCCGCGCAGGGT 708
QY 181 AASPSERGLYGILPROLEUVALCYSAANGINSERLEUNGILYILESEERTPGIYGLN 200
DB 709 GACTCGGGGGGCTCTGTGTGTACACAGTCTCTTCAAGGATATATCTCGGGGCGAG 768
QY 201 AASPPOCYSAIAILETHARGLYSPROGLYVALIYRTHLVSAVALCYSLYSTYRVALASP 220
DB 769 GATCGGTGTGCATACCCGAAAGCCTGTGTCTACACGAAGTCTGCAAAATATGTGAC 828
QY 221 TPTILEGILGLUTHMETLYSASANSN 229
DB 829 TGGATCCAGAGACATGAAGAACAT 855

RESULT 10
ABL88175
ID ABL88175 standard; cDNA; 1204 BP.

XX ABL88175;

XX 16-MAY-2002 (first entry)

DE Human PRO1279 cDNA sequence SEQ ID NO:207.

KW Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
KW vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.

OS Homo sapiens.

PN WO2002006930-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US19692.

XX 23-JUN-2000; 2000US-213637P.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 25-JUL-2000; 2000US-220664P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-064365P.

XX 23-AUG-2000; 2000WO-US23352.

XX 24-AUG-2000; 2000WO-US23328.

XX 07-SEP-2000; 2000US-230978P.

XX 18-SEP-2000; 2000US-0664610.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-249222P.

XX 08-NOV-2000; 2000US-0709238.

XX 08-NOV-2000; 2000WO-US30952.

XX 10-NOV-2000; 2000WO-US30873.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000US-0747259.

XX 20-DEC-2000; 2000WO-US34956.

XX 22-JAN-2001; 2001US-0767609.

XX 28-FEB-2001; 2001US-0796498.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2001; 2001WO-US06666.

XX 09-MAR-2001; 2001US-0802706.

XX 14-MAR-2001; 2001US-0808689.

XX 22-MAR-2001; 2001US-0816744.

XX 05-APR-2001; 2001US-0828366.

XX 10-MAY-2001; 2001US-0854208.

XX 10-MAY-2001; 2001US-0854280.

XX 25-MAY-2001; 2001US-0866028.

XX 25-MAY-2001; 2001US-0866034.

XX 25-MAY-2001; 2001WO-US17092.

XX 30-MAY-2001; 2001US-0870574.

XX 30-MAY-2001; 2001WO-US17443.

XX 01-JUN-2001; 2001WO-US17800.

XX (GETH) GENENTECH INC.

XX PA

XX PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A;

XX PI Godowski PJ, Gunney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

XX PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX DR WPI; 2002-090516/12.

XX DR P-PSDB; ABB84920.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 2; Fig 207; 565pp; English.

CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarction, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.

SO Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:
 Pred. No.: 5,04e-105 Length: 1204
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABL88175 (1-1204)

QY 1 IIEIIILYGLYHEGLUCYSYSPROHILASERGLPROTRPGLMAALALEUPHEGLU 20
 DB 169 ATCATAGAGGGTTCCAGTGCAAGCTCACTCCACCCCTGGAGCAGCAGCCCTTCCGAG 228
 QY 21 LYSYTHARGLEULEUCYSGLYALATHRLEULEALPROARGTRPHEULEUTHRALA 40
 DB 229 AAGACCGGCTACTGTGGGGGAGCGCTCATGCCCCCAGATGCTCTTGACAGACGC 288
 QY 41 HSYSEULEULYSPROARGTRYILEVALHISLEULYGLNHISANLEULYSGIULU 60
 DB 289 CACTGGCTCAAGCCCGCTACATAGTTCACTGGGAGACACCTCCAGAAAGAGGAG 348
 QY 61 GLYCYGLUGLINTHRARGTHRALATHRGLUSERPHEPROHISPROGLYPHEANSEN 80
 DB 349 GGCTGTGACGACACCGGACGACGACTGCTTCCACCCCGCTTCAACACACAC 408
 QY 81 LEUPROASULYSPHISARGAENAPIIEMETLEUVALYSEMERALASERPROVALSAR 100
 DB 409 CTCGCCAAGACACGACCGCAATGACATCATGCTGTGAAGTGCATGCGCAGCTTCC 468
 QY 101 IIEHTRTPALAVALARPPOLEUTHRLEUSERSERARGCYSEVALTHRALAGLYTHR 120
 DB 469 ATACCTGGGGCTGTGGACCCCTCACCTCTCTCAACGCTGTCTACTGTGGACACAC 528
 QY 121 CYSEULILESERGLYTRPGLYSERTHRSESERPROGLHLEUARGLEUPROHISHT 140
 DB 529 TGGCTCATTTCCGGGCTGGGGGACAGCTCAGCCCCCAGCTTACGCTCCACACCTTG 588
 QY 141 ARGCYSEVALASNIIEHTRILEIIEGLIHISGLINLYSEGLASNAALATYRPROGL 160
 DB 589 CGATGGCCCAACATCCCATTCATTGACACCAAGATGTGAGAACCCCTTACCCCGGCAAC 648
 QY 161 IIEHTRASPETHMEVALCYSEVALSERVALINGIULYGLYLYSASPERSCYSGINGLY 180
 DB 649 ATCAGACAGACCATGTGTGTGTCGACGCGAGAAAGGGGAGGAGACTCCGCGAGGT 708
 QY 181 AAPPSEGLYGLYPROLEUVALCYSEANGLINSEULEINGLYIIEIIESERTTPGLYGIN 200
 DB 709 GACTCGGGGGCCCTCTGTGTGTACACGAGTCTTCAAGGACATATATCTCGGGGCCAG 768

QY 201 AAPPICYSALAIIEHTRARGLYSPROGLYVALTYRTHRYSEVALCYSELYTYRVALASP 220
 DB 769 GATCCGTGTGCGATACCCGAAAGCTGTGTCTACACCAAAAGTCTGCAATATGTGCAC 828

QY 221 TRPILIEGLINLUHTRMETLYSANBAN 229
 DB 829 TGGATCCAGAGACGATGAAGAAACAT 855

RESULT 11

ABK33628
 ID ABK33628 standard; cDNA; 1204 BP.

AC ABK33628;

DT 08-MAY-2002 (first entry)

DE cDNA encoding human PRO protein, Seq ID No 185.

KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;

KW breast cancer; prostate tumour; rectal tumour; liver tumour;

KW pericyte cell proliferation; chondrocyte cell proliferation;

KW tumour necrosis factor-alpha; gene; ss.

OS Homo sapiens.

PN WO200208288-A2.

PD 31-JAN-2002.

PF 29-JUN-2001; 2001WO-US21066.

PR 20-JUL-2000; 2000US-219556P.

PR 25-JUL-2000; 2000US-220585P.

PR 25-JUL-2000; 2000US-220605P.

PR 25-JUL-2000; 2000US-220607P.

PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220638P.

PR 25-JUL-2000; 2000US-220664P.

PR 26-JUL-2000; 2000US-220893P.

PR 28-JUL-2000; 2000WO-US20710.

PR 23-AUG-2000; 2000WO-US23522.

PR 14-AUG-2000; 2000WO-US23328.

PR 15-SEP-2000; 2000US-000000P.

PR 10-NOV-2000; 2000WO-US30873.

PR 28-NOV-2000; 2000US-253646P.

PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000US-0747259.

PR 20-DEC-2000; 2000WO-US34956.

PR 28-FEB-2001; 2001WO-US06520.

PR 10-MAY-2001; 2001US-0854280.

PR 25-MAY-2001; 2001WO-US17092.

(GETH) GENENTECH INC.

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

DR WPI; 2002-172001/22.

DR P-PSDB; AAU83684.

PT One hundred and twenty two nucleic acids encoding PRO polypeptides,

PT useful for treating a PRO related disorder and for diagnosing tumours

PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal

PT tumour or liver tumour -

PS Claim 2; Figure 185; 359pp; English.

CC The invention relates to one hundred and twenty two nucleic acids

CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides

CC encode human secreted proteins. The PRO nucleic acids, polypeptides,

CC agonists and antagonists are useful for treating a PRO related disorder.

CC The PRO polypeptides are useful for diagnosing tumours, especially lung

CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK3536-ABK3567 represent human
CC PRO protein coding sequences of the invention.

XX
SQ Sequence 1204 BP, 306 A, 364 C, 294 G, 240 T, 0 other;

Alignment Scores:

Pred. No.:	5,04e-105	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-856-320A-2_copy_54_282 (1-229) x ABK35628 (1-1204)

QY 1 ILEILEVSGLYPHEGLUCYSYSPROHISERGINPROTIRGINALALEUPHEGLU 20
DB 169 ATCATCAAGGGGTTCCAGTCAAGCCTCACTCCAGCCTCGACAGCACCCCTGTTCCAG 228
QY 21 LVSTHARGLLEUCYSGIYLAATHRLEUILEAIPROARGTRILEUETHRALALA 40
DB 229 AAGACCGGCTACTCTGTGGGGCGAGCGCTCATCGCCCAAGATGGCTCTTGACAGCAGC 288
QY 41 HISCYSLLEUYSPROARGTRILEVALHISLEUGLYGNIHISASNLEUINLSGLU 60
DB 289 CACTGCGCTCAAGCCCGCTACATAGTTCACTGGGGCAGACACCACTCAGAAAGAGAG 348
QY 61 GLYCYSGIUGLINTHARGTHRILATHRGUSERPHEPRHISIPROGLYPHEASNLSER 80
DB 349 GGCTGTGACAGACCCGAGCAGCCAGCTGCTCTTCCCGCCCGCTTCAACACAGC 408
QY 81 LEUPROASNLYASPHISARASNAPLILEMETLEUVALYMETALASERPROVALSER 100
DB 409 CTCGCCAACAAGACCCAGCATGATGATGCTGTAAGATGGCATCGCAGTCTCC 468
QY 101 ILEHTRIPALVALARGPROLEUTHRIEUSERSERARGCYSAVALTHRALGLYTHRSER 120
DB 469 ATCACCTGGGCTGTGGACCCCTCACTCTCTCCTCAGCTGTGCTACTGTCGACAGC 528
QY 121 CYSEULLESERGLYTRPGLYSERTHRSERPROGINLEUARGLEUPROHISTHRIEU 140
DB 529 TCCCTCATTTCCGGCTGGGGCAGACGTCACCCCACTTACGCTGCTTACACCTTG 588
QY 141 ARGCYSAALASNILETHRIELLEGLIUSIINLYSCYGLIASNALATYRPROGLYASN 160
DB 589 CCAATGGCCCAATCACTCACTTACGACCAAGAGTGTGAAGACCCCTACCCCGGCANC 648
QY 161 ILEHTRASPTRHMEVALCYSAIASERYALINGIUGLYLYASPSERCYSGINGLY 180
DB 649 ATCACAGACACCATGGTGTGTGCCAGCGTCAGAGAAAGGGGCGAGACTCTGCCAGGAT 708
QY 181 ASPSERGLYGLYPROLEUVALCYSAASNGINSEIRLEUINGLYTILELESETRPGLYGIN 200
DB 709 GACTCCGGGGCCCTCTGTGTGTAAACGCTCTTCAAGGATTAATCTCCGGGGCCAG 768
QY 201 AAPPROCYSAALILETHRARGLYSPROGLYVALTYRTHLYVALCYSLSTYRVALASP 220
DB 769 GATCGGTGTGCCATACCCGAAAGCTGTGTCTACAGAAAGTCTGCAAAATATGTGAC 828
QY 221 TPIPLEINGIUTHRMELYSASNAN 229
DB 829 TCGATCCAGAGACGATGAAGAAAT 855
RESULT 12

ACAA03855
ID ACAA03855 standard; cDNA; 1204 BP.
AC ACAA03855;
XX
XX
DT 23-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #253.
XX
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytoskeletal; gene; ss.
XX
OS Homo sapiens.
XX
XX
XX US2003036180-A1.
XX
XX 20-FEB-2003.
XX
XX
XX 09-MAY-2002; 2002US-0143114.
XX
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00326.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.

02-MAR-2000; 2000MO-US05746.
 02-MAR-2000; 2000MO-US05841.
 10-MAR-2000; 2000MO-US06319.
 15-MAR-2000; 2000MO-US06884.
 20-MAR-2000; 2000MO-US07377.
 21-MAR-2000; 2000MO-US07532.
 30-MAR-2000; 2000MO-US08439.
 17-MAY-2000; 2000MO-US13705.
 32-MAY-2000; 2000MO-US14042.
 02-JUN-2000; 2000MO-US14941.
 28-JUL-2000; 2000MO-US15264.
 11-AUG-2000; 2000MO-US20710.
 23-AUG-2000; 2000MO-US22031.
 24-AUG-2000; 2000MO-US23328.
 08-NOV-2000; 2000MO-US30952.
 10-NOV-2000; 2000MO-US30873.
 01-DEC-2000; 2000MO-US32678.
 20-DEC-2000; 2000MO-US34956.
 28-FEB-2001; 2001MO-US06520.
 01-MAR-2001; 2001MO-US06666.
 25-MAY-2001; 2001MO-US17092.
 01-JUN-2001; 2001MO-US17800.
 20-JUN-2001; 2001MO-US19692.
 22-JUN-2001; 2001MO-US20116.
 29-JUN-2001; 2001MO-US21066.
 09-JUL-2001; 2001MO-US21735.
 20-DEC-2000; 2000US-0747259.
 28-FEB-2001; 2001US-0796498.
 09-MAR-2001; 2001US-0802706.
 14-MAR-2001; 2001US-0806889.
 22-MAR-2001; 2001US-0816744.
 05-APR-2001; 2001US-0828366.
 10-MAY-2001; 2001US-084208.
 10-MAY-2001; 2001US-0854280.
 18-MAY-2001; 2001US-0860216.
 25-MAY-2001; 2001US-0866028.
 01-JUN-2001; 2001US-0866034.
 05-JUN-2001; 2001US-0872035.
 14-JUN-2001; 2001US-0874503.
 19-JUN-2001; 2001US-0882636.
 21-JUN-2001; 2001US-0886342.
 18-JUL-2001; 2001US-0887879.
 06-AUG-2001; 2001US-0908827.
 09-AUG-2001; 2001US-0924419.
 16-AUG-2001; 2001US-0927796.
 19-DEC-2001; 2001US-0931836.
 (GENTH) GENENTECH INC.
 Baker KP, Beresini M, DeGeorge L, Desnoyers L, Filvaroff E, Gao W, Gerlitsen WE, Goddard A, Godowski PJ, Gurney AL, Sherwood S, Smith V, Stewart TA, Tumas CK, Watanabe CK, Wood WI, Zhang Z, WPI: 2003-332040/31.
 P-PSDB; AB066822.
 New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification
 Claim 2: Fig 505; 660pp; English.

the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ACA03603-ACA03877 represent CDNAs encoding the human PRO polypeptides of the invention.
 Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipdsidentry.html.
 Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 Alignment Scores:
 Pred. No.: 5,04e-105 Length: 1204
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-09-856-320A-2_COPY_54_282 (1-229) x ACA03855 (1-1204)
 1 IleIleIysGlyPheGluCysIysProHisSerGlnProTyrGlnAlaAlaLeuPheGlu 20
 169 ATCATCAAGGGGTTGAGTGCAGGCTCACTCCAGCCCTGGCAGGACCCCTGTCGAG 228
 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrLeuLeuThrAlaAla 40
 229 AAGAGCGGCTACTCTGTGGGGCGAGCGCTCACTCCGCCAGATGCTCCTGACAGAGCC 288
 41 HisCysLeuIysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnIysGlu 60
 289 CACTGCTCAAGCCCGCTGACATGATGCTCACTGCGGCGAGCAACCTCCAGAGAGAGG 348
 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
 349 GGCTGTGAGCAGACCCGCGAGACCCCTAGTCTTCCCCACCCCGGCTTCAACAGAGC 408
 81 LeuProAsnIysAspHisArgAsnAspIleMetLeuValIysMetAlaSerProValSer 100
 409 CTCGCCAACAAGACACCGCATCATCATGCTGTGAAGATGCATCCGCACTCC 468
 101 IleThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
 469 ATCACTGGGCTGTGCGACCCCTCACTCTCCACCTGTGTCACTGCTGGCAGCAGC 528
 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
 529 TGCCTCATTTCCGGCTGGGGGAGCAGCTCAAGCCCGCCAGTTACGCTCTCAGCCTTG 588
 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnIysCysGluAsnAlaTyrProGlyAsn 160
 589 CGATCGCCCAATACCATCATTTAGAGCAGCAGAGTGTGAAGACGCTACCCCGGCAAC 648
 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyIysAspSerCysGlnGly 180
 649 ATCAGAGACACCATGTGTGTGCGAGCTGTGAGAGAGGGGCGAGAGCTCTCCAGAGGT 708
 181 AspSerGlyIysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGln 200
 709 GACTCCGGGGGCTTGTGTGTGTGTAACAGTCTTTCAGGCAATATCTCTGGGGCAG 768
 201 AspProCysAlaIleThrArgIysProGlyValTyrThrIysValCysIysTyrValAsp 220
 769 GATCGGTGTGAGATACCCGAAAGCTGTGTCTTCAAGAAAGTCTCAAAATATGTGAC 828
 221 TrpIleGlnGluThrMetIysAsnAsn 229
 829 TGGATCCAGAGAGCATGACATGACAAAT 855
 RESULT 13

ACA04276
ID ACA04276 standard; cDNA, 1204 BP.
XX
AC ACA04276;
XX
DT 27-MAY-2003 (first entry)
XX
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 505.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioresactor; tumour.
XX
OS Homo sapiens.
XX
PN US2003032155-A1.
XX
PD 13-FEB-2003.
XX
PF 03-MAY-2002; 2002US-0137865.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24655.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US06615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 22-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 05-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.

PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
PI Gertlisen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-331925/31.
DR P-PSDB; ABU67098.
XX
XX New secreted and transmembrane nucleic acids and polypeptides,
PT designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer
XX
XX
XX Claim 2; Fig 505; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid
CC further comprises the full-length coding sequence of the DNA deposited
CC under American Type Culture Collection (ATCC) accession number in a list
CC given in the specification. Also included are vectors and host

CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumor necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumor in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence encodes a PRO protein of the invention.

XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:

Pred. No.: 5.04e-105 Length: 1204
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ACA04276 (1-1204)

QY 1 llelellyg1yPheglucyslpsProhisSerglnProtrpGlnAlaIaleupheglu 20
 DB 169 ATCATCAAGGGGTTCAGTGCAGCAAGCTCTCCACGCTCGGAGGACGCTGTTCCGAG 228
 QY 21 lvsfthArgleuLeuCySglYalathrlleu1lealaproargftrpleuLeuthralaala 40
 DB 229 AAGACCCGGCTACTGTGGGGGAGCGCTCATGCGCCCAAGATGCTCTGACAGAGC 288
 QY 41 HisCyLeuLysProArgTrpTrileValHisleuGlyGlnHisAsnleuGlnysgluGlu 60
 DB 289 CACTGCTCAAGCCCGCTACAAAGTTCACTGGGGGACACCAACTCCAGAGGAGGAG 348
 QY 61 GlyCyGluGlnthArgTrpThralatnrgLuserPheProhisSProglyPheAsnAsnser 80
 DB 349 GGCTGTGACAGACCCCGGACAGCACTGAGTCTTCCCAACCCCGGCTTCAACAGAC 408
 QY 81 LeuProAsnLysAspHisArgAsnAspGllIemeltLeuValysWecalaSerProValSer 100
 DB 409 CTCCCCCAAGCAAGACCGCAATGATCATGCTGTGAGATGAGATGCGCATCGCCAGCTCC 468
 QY 101 lleThTrpAlaValargProleuThrluserSerArgCyValThrlaGlyThrser 120
 DB 469 ATCACTGGAGCTGTGGACCCCTCAACCTCTCTCAAGCTGTGTCACTGTGACACAGC 528
 QY 121 CysLeuIleSerglyYTrpGlySerThrSergSerPrgGlnLeuargLeuProhisThrlau 140
 DB 529 TCCCTCATTTCCGGCTGGGGGAGCAAGTCAAGCCCACTTACGCTGCTCAACACTTG 588
 QY 141 ArgCySAlaAsn1leThrlle1legluHisGlnLysCySgluAsnAlaTytrProglYasn 160
 DB 589 CGATGGCCCAACATCCATCATTTGAGCACCAGAAAGTGTGAGAACCCCTACCCGCAAC 648
 QY 161 lleThAspThMerValCysAlaSerValGlnGluGlyLysAspSerCySglnGly 180
 DB 649 ATTCACGAGACCATGTGTGTGTGCACAGCGGAGGAAGGGGGGAGACCTCCGACGGGT 708
 QY 181 AspSerglyGlyProleuValCysaenglnSerLeuGlnGly1leIleSerTrpGlyGln 200

DB 709 GACTCGGGGGCCCTCTGTGTGTACCAAGCTCTTCAAGGATATATCTCGGGCCAG 768
 QY 201 AppProCySAla1leThrArgLysProglYal1TyThrlvsAlCysLysTyrrValasp 220
 DB 769 GATCCGTGTGCATCAACCGGAAGCTGTGTCTACAGAAAGTCTGCAAAATATGTGAC 828
 QY 221 TrpIleGlnGluThMerLysAsnAsn 229
 DB 829 TGGATTCAGAGACGATGAGAACANT 855
 RESULT 14
 ABX89393
 ID ABX89393 standard; cDNA; 1204 BP.
 AC ABX89393;
 AC 13-MAY-2003 (first entry)
 DT
 XX
 XX
 DE DNA encoding novel secreted and transmembrane protein PRO1279.
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumor; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosum; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
 OS Homo sapiens.
 XX
 XX US2003017563-A1.
 PN
 XX
 PD 23-JAN-2003.
 XX
 PF 07-MAY-2002; 2002US-0140808.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US34956.
PR 20-DEC-2000; 2000WO-US34958.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0806889.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 01-JUN-2001; 2001US-0866034.
PR 05-JUN-2001; 2001US-0872035.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
PI Geriltsen ME, Goddard PJ, Gunney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX

DR WPI: 2003-148238/14.
DR P-PBDB: ABUS9903.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments -
XX
XX Claim 2; Fig 505; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum. AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or Crohn's
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC sequence encodes a novel human PRO protein.
XX
XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
SQ
XX
XX Alignment Scores:
XX Pred. No.: 5.04e-105 Length: 1204
XX Score: 1258.00 Matches: 229
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: Gaps: 0
XX
XX US-09-856-320A-2_COPY_54_282 (1-229) x ABX89393 (1-1204)
QY 1 IletlelysglypnehuCyalsProHisSerGlnProTPGlnAlaAlaLeuPheGlu 20
DB 169 ATCATCAAGGGGCTTCAAGTCAAGCTCACCACCCGCTTGGACGAGCCCTGTTGAG 228
QY 21 LysThrArgLeuLeuCyGlyAlaThrIleuAlaAProArgTPleuLeuThrAlaAla 40
DB 229 AAGACGCGGCTACTGTTGGGGCGACGCTCATCCGCCCAATGAGCTCTGACGACGCC 288
QY 41 HisCysLeuLysProArgTYrIleValHisIleuLysGlnHisAsnLeuGlnLysGlu 60
DB 289 CACTGCCTCAAGCCCGCTACATGTTCACTGGGGCGACCAACCTTCCAAAGGAGAG 348
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
DB 349 GGTCTGACGACGACCCGACGACGACCTGAGCTTCCGCCGCCGCTTCAACACAGC 408
QY 81 LeuProAsnLysAspHisArgAsnAspLleuMetLeuValLysMetAlaSerProValSer 100
DB 409 CTCGCCAACAAGACCAACCGCAATGACATCATGCTGTGAAGATGAGCATCCGACGTCTCC 468
QY 101 IleThrTrpAlaValAlaGProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120

Db ATCAGCTGGGCTGTGACCCCTCACCTCTCTCTCACGCTGTGTCACTGCTGGCACGAG 528
 QY CysLeuIleSerGlyTyrPglYserThrSerSerProGlnLeuArgLeuProHisThrLeu 140
 Db TGGCTATTTCGGGCTGGGGGACACGCTCCAGCCCGAGTACGCTGCTCACACCTTG 588
 QY ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
 Db CGATGGGCCAACATCATCATCATGAGCACCAAGGTGAGAACCCCTTACCCCGGCAAC 648
 QY IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180
 Db ATCAGACAGACACCATGTGTGTGTCAGAGTCAGAAAGGGGGCAAGAGACTCTCCAGGGT 708
 QY AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGln 200
 Db GACTCCGGGGGCGCTGTGTGTGTACCACTCTCTTCAAGGCATTAATCTCTGGGGCCAG 768
 QY AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 220
 Db GATCCTGTGCGATCATCCGAAAGCCTGTGTCTTACACCAAGTCTGCAATATGTGAC 828
 QY TTPILeGlnGluThrMetLysAsnAsn 229
 Db TGGATCCAGAGACGATGAAGAACAT 855
 RESULT 15
 ABA83372 standard; cDNA; 1292 BP.
 ABA83372;
 07-FEB-2002 (first entry)
 Human secreted protein gene 179 SEQ ID NO:189.
 Human: secreted protein; immunomodulatory; antisclerotic; anti-HIV;
 dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
 cytostatic; caldant; vascular; anti-angiogenic; ophthalmological;
 neuroprotective; nootropic; anticonvulsant; antialzheimer's; vulnary;
 antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
 multiple sclerosis; systemic lupus erythematosus; HIV infection; healing;
 human immunodeficiency virus; hyperproliferative disorder; wound healing;
 Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis;
 Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
 corneal graft neovascularisation; diabetic retinopathy; regeneration;
 neurological disorder; Huntington's chorea; Alzheimer's disease;
 Parkinson's disease; infectious disease; ss.
 OS Homo sapiens.
 XX WO200162891-A2.
 PN 30-AUG-2001.
 PD 21-FEB-2001; 2001WO-US05614.
 PF 24-FEB-2000; 2000US-184836P.
 PR 29-MAR-2000; 2000US-193170P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferris AM, Fan P;
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
 PI Zeng Z, Greene JW;
 XX WPI, 2001-625724/72.
 DR P-PSDB; ABB50479.
 PT Nucleic acids encoding 207 human secreted polypeptides, useful for

PT Preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
 disease and diabetic retinopathy -
 XX PS Claim 1, Page 1032; 1533pp; English.
 XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.
 CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
 CC anti-HIV; cytostatic; caldant; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimer's; vascular;
 CC antiparkinsonian; antimicrobial; and vulnary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis) and diabetic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
 CC ABA83193 and ABB50300 represent sequences used in the exemplification of
 CC the present invention.
 XX SQ Sequence 1292 BP; 319 A; 387 C; 329 G; 253 T; 4 other;
 Alignment Scores:
 Pred. No.: 5,52e-105 Length: 1292
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-09-856-320A-2_COPY_54_282 (1-229) x ABA83372 (1-1292)
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 Db 270 ATCATCAAGGGGTTGAGAGCAAGCCTCACTCCAGCCTGGACAGACCTGTTCGAG 329
 QY 21 LysThrArgLysLeuCysGlyValaThrLeuIleAlaProArgTyrLeuThrAla 40
 Db 330 AAGACGGGCTTCTGTGGGGCGACGCTCATGCCCCAGATGGCTCTGACAGAGCC 389
 QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlnGlnHisAsnLeuGlnLysGln 60
 Db 390 CACTGCTCAAGCCCGGCTACACTGTTACCTGGGGGACAGACACTCCAGAAAGAGAG 449
 QY 61 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 80
 Db 450 GGCTGTGAGACACCGGACAGCAGCTGAGTCTTCCCAACCCGGCTTCAACACAGC 509
 QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
 Db 510 CTCCCAACAAAGACACCGGACATGATGCTGGTGAATGACATGCGCAAGTCTCC 569
 QY 101 IleThrTyrAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
 Db 570 ATCAGCTGGGCTGTGCGACCCCTCACTCTCTCACTGCTGTGCTGCTGCTGCTG 629
 QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
 Db 630 TGYCTCATTTCCGGCTGGGGGACAGCGTCCAGCCCGGAGTTACGCTGCTCACACCTTG 689
 QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
 Db 690 CGATGGGCCAACATCATCATCATGAGCACCAAGGTGAGAACCCCTTACCCCGGCAAC 749
 QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180
 Db 750 ATCAGACAGACACCATGTGTGTGTCAGAGTCAGAAAGGGGGCAAGAGACTCTCCAGGGT 809

QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
 Db 810 GACTCCGGGGGCCCTCTGCTGTGTAACCACTCTTCAAGCATTAATCTCTGGGGCCAG 869
 QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 220
 Db 870 GATCCGTGTGCGATCACCCGAAAGCCTGTGTGTACACGAAAGTCTGCNAATATGTGTGAC 929
 QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
 Db 930 TCGATCCAGAGACGATGAAGAACAAT 956

Search completed: October 23, 2003, 15:58:15
 Job time : 260.855 secs

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Sequence:

MÖRLRWLRDM KSSGRGLTAA KPGARSSPL QAMRIQLIL LALATGLVGG ETRIIRKGFEC
KPHSQPWQAA LFEKTRLLCG ATLAPRWLL TAAHCLKPRY IVHLGQHNLO KEEGCEQTRT
ATESFPHPGF NNSLPNKDHR NDIMLVKMAS PVSITWAVRP LTLSSRCVTA GTSCGISGWG
STSSPQLRLP HTLRCANITL IEHQKCEENAY PGNITDTMVC ASVQEGGKDS CQGDSSGGPLV
CNGSLQGIS WQDPCAATR KPGVYTKVCK YVDWIDQETMK NN

PROSITE Release 18.10, of 12-Oct-2003

>PDOC00001 ASN_GLYCOSYLATION N-glycosylation site [pattern] [Warning: pattern with a high probability of occurrence].

131 - 134 NNSL
197 - 200 NITI
213 - 216 NITD
242 - 245 NQSL

>PDOC00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site [pattern] [Warning: pattern with a high probability of occurrence].

13 - 15 SGR
164 - 166 SSR
192 - 194 TIR
259 - 261 TRK
278 - 280 Tmk

>PDOC00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site [pattern] [Warning: pattern with a high probability of occurrence].

120 - 123 TAT
199 - 202 TIE
222 - 225 SVQE

>PDOC00008 MYRISTYL_N-myristoylation site [pattern] [Warning: pattern with a high probability of occurrence].

16 - 21 GLTAK
46 - 51 GLVGE
114 - 119 GCEQTR
226 - 231 GSKDSC
252 - 257 GQDPCA

>PDOC00124 PS50240 TRYPSIN_DOM Serine proteases, trypsin domain [profile].

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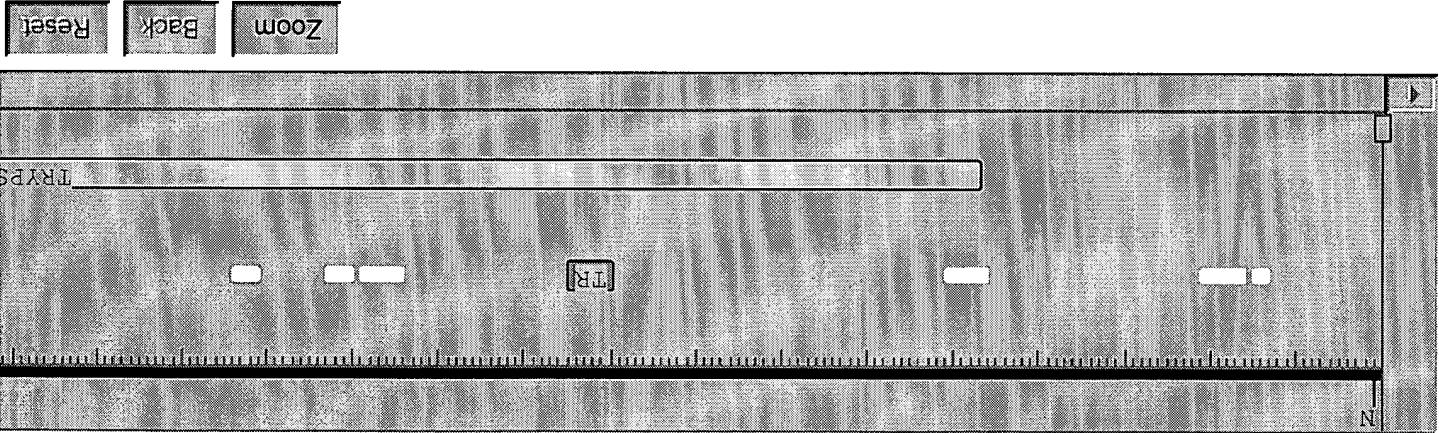
47 - 280LVGGEtrikgfECKPHSQPWQALFEKT-RLTCGATLIAPRWLLTAAHCLKPR-----Y
IVHLGQHNLOKKEEGCEQTRTATESFPHPGFNslpNKDHRNDIMLVKMASPVSITWAVRP
LTL--SSRCVTAGTSCGISGWSSTSPqLRLPHHTLRCANITIIIEHQKC-ENAYPGNITDT
MVCASVQEGEKDSCQGDSDSGGPLVC-----NQSLQGIISWGDPCAITRKPGVYTKVCCKYVD
WIOETMK

>PD0C00124 PS00134 TRYPsin_HIS Serine proteases, trypsin family, histidine active site [pattern].
90 - 95 LTAHAC

>PD0C00124 PS00135 TRYPsin_SER Serine proteases, trypsin family, serine active site [pattern].
229 - 240 DScqGDSDSGGPLV

Graphical summary of hits (java applet)

Click on items to see a description. Drag the two red cursors to select a zoom region.



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